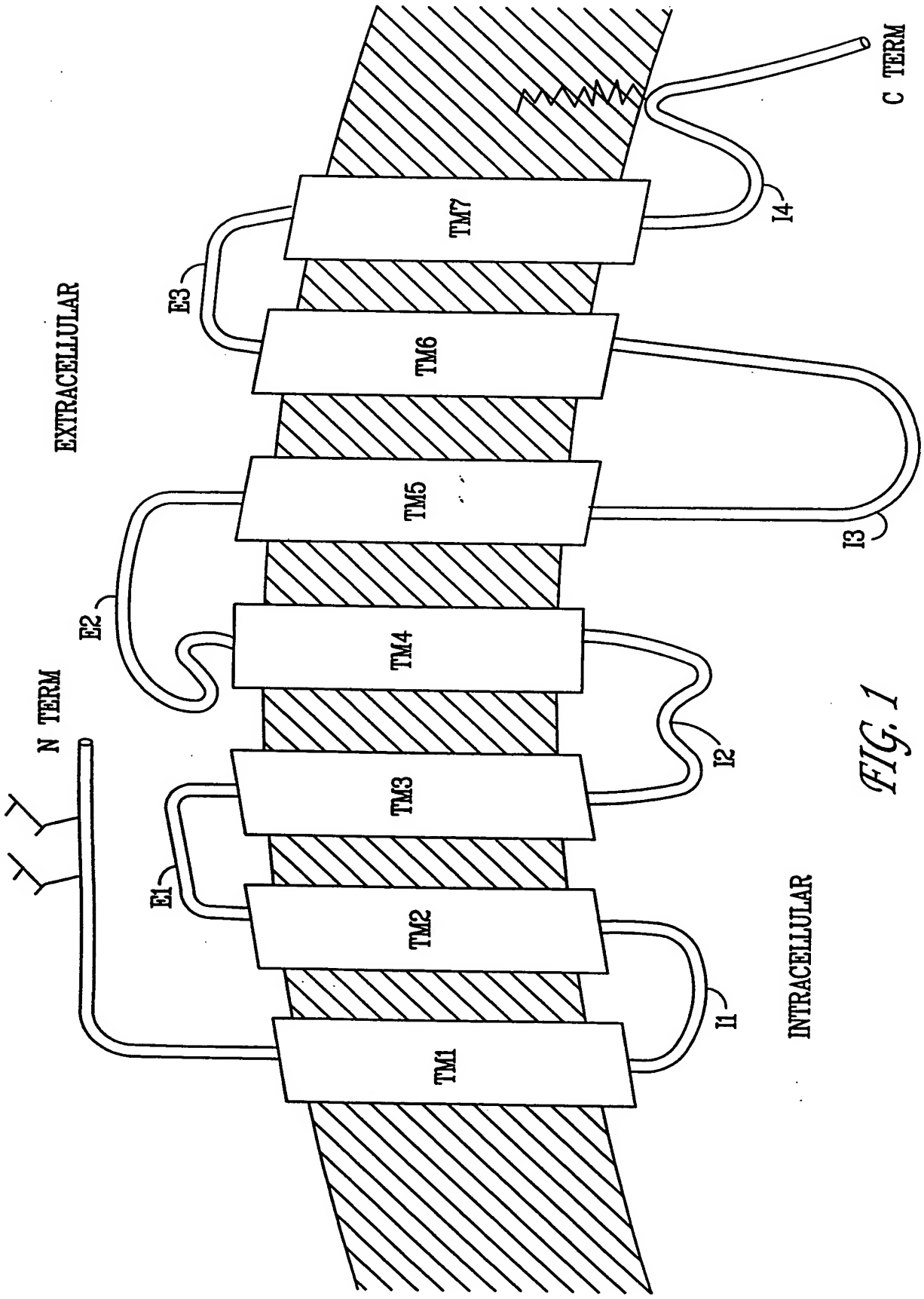

EXTRACELLULAR
N TERM
C TERM
INTRACELLULAR
TM1
TM2
TM3
TM4
TM5
TM6
TM7
E1
E2
E3
I1
I2
I3
I4

FIG. 1

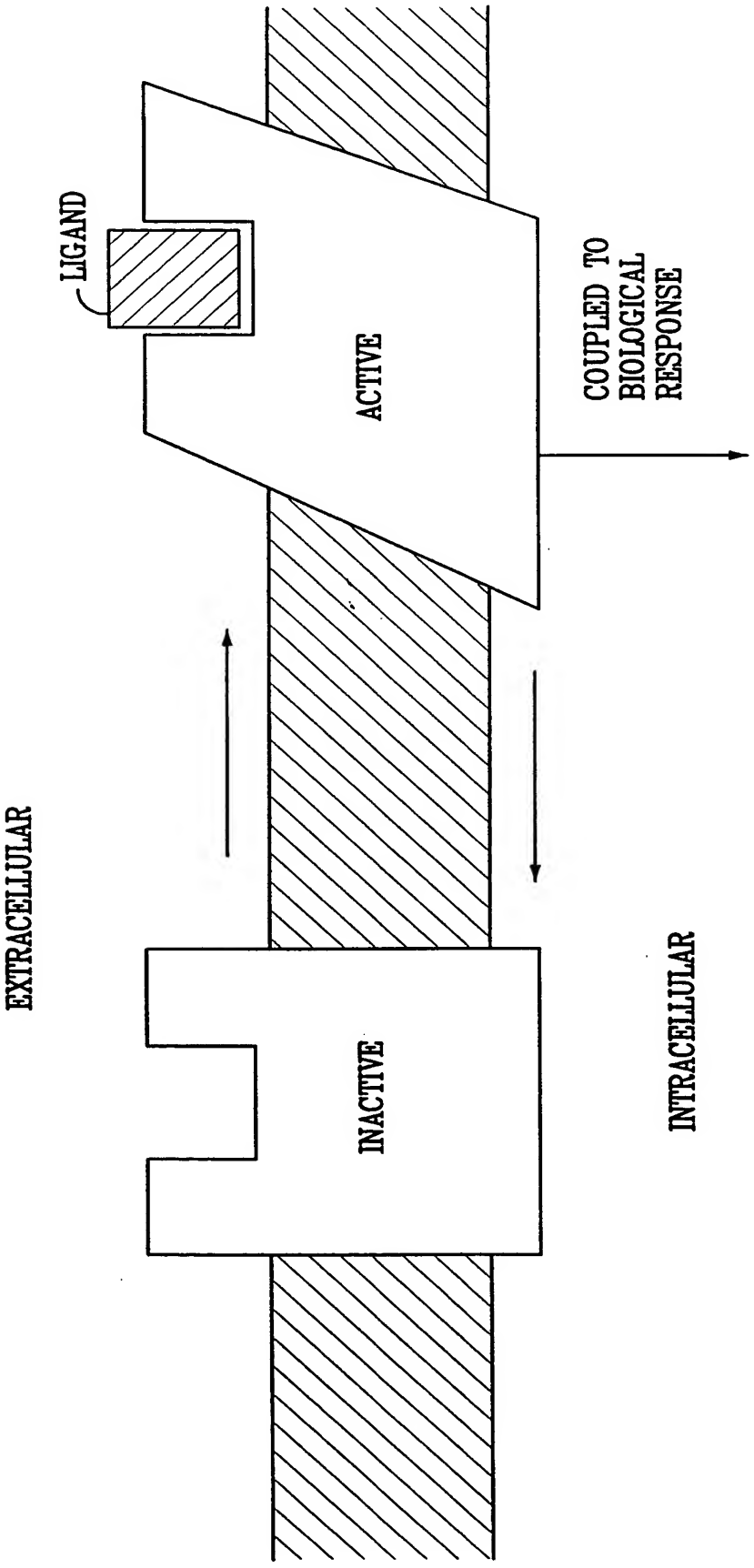

LIGAND
ACTIVE
COUPLED TO BIOLOGICAL RESPONSE
EXTRACELLULAR
INACTIVE
INTRACELLULAR

FIG. 2

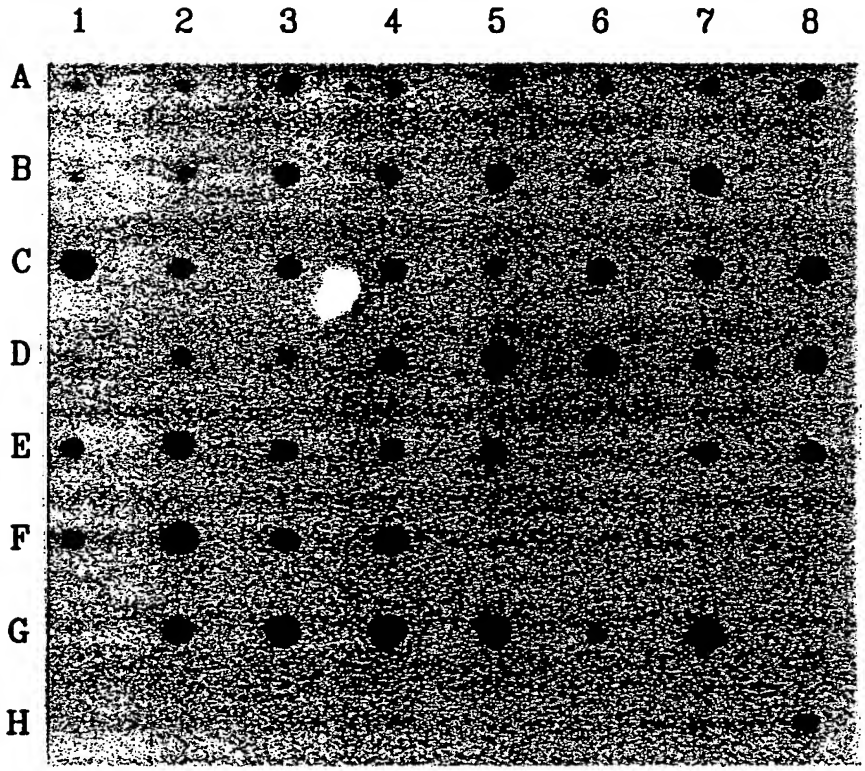


FIG. 3

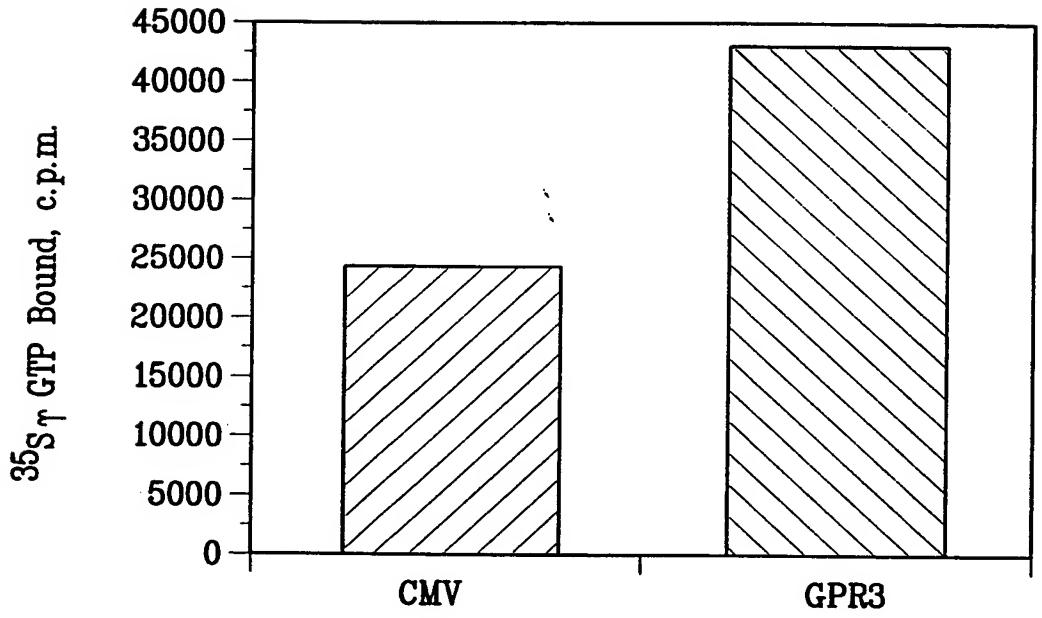
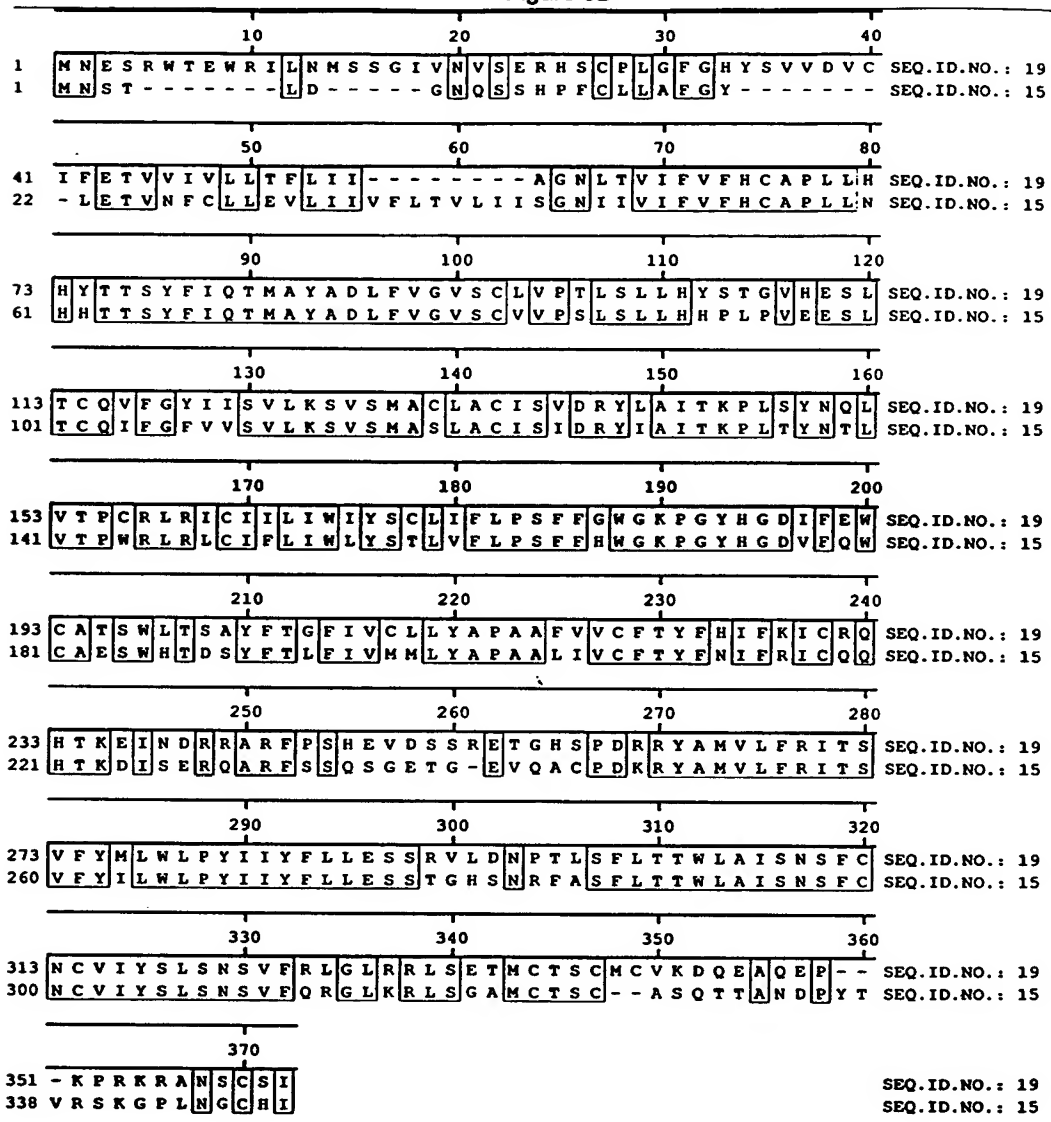

45000
40000
35000
30000
25000
20000
15000
10000
5000
0
$^{35}S\gamma$ GTP Bound, c.p.m.
CMV
GPR3

FIG. 4

Figure 5A

10 30 40
1 MM----------WGAGS SEQ.ID.NO.: 46
1 MNASAASLNDSQVVVVAAEGAAAAATAAGGPDTGEWGPPA SEQ.ID.NO.: 47
1 MN------EDLKVNL----------SGL SEQ.ID.NO.: 48
50 60 70 80
8 PLAWLSAGSGNVNVSSVGPAEGPTGPAAPLPSPKAWDVVL SEQ.ID.NO.: 46
41 AAA-LGAGGGANGSLELSSQLSAGPPGLLLPAVNPWDVLL SEQ.ID.NO.: 47
13 PRDYLDAAAAENISAAVSSRVPAVEPEPEL-VVNPWDIVL SEQ.ID.NO.: 48
90 100 110 120
48 CISGTLVSCENALVVAIIVGTPAFRAPMFLLVGSLAVADL SEQ.ID.NO.: 46
80 CVSGTVIAGENALVVALIASTPALRTPMFVLVGSLATADL SEQ.ID.NO.: 47
52 CTSGTLISCENAIVVLIIFHNPSLRAPMFLLIGSLALADL SEQ.ID.NO.: 48
130 140 150 160
88 LAGLGLVLHFAAVFCIGSAEMSLVLVGVLAMAFTASIGSL SEQ.ID.NO.: 46
120 LAGCGLILHFVFQYLVPSETVSLLTVGFLVASFAASVSSL SEQ.ID.NO.: 47
92 LAGIGLITNFVFAYLLQSEATKLVTIGLIVASFSASVCSL SEQ.ID.NO.: 48
170 180 190 200
128 LAITVDRYLSLYNALTYYSETTVTRTYVMLALVWGGALGL SEQ.ID.NO.: 46
160 LAITVDRYLSLYNALTYYSRRTLLGVHLLLAATWTVSLGL SEQ.ID.NO.: 47
132 LAITVDRYLSLYYALTYHSERTVTFTYVMLVMLWGTSICL SEQ.ID.NO.: 48
210 220 230 240
168 GLLPVLAWNCLDGLTTCGVVYPLSKNHLVVLAIAFFMVFG SEQ.ID.NO.: 46
200 GLLPVLGWNCLAERAACSVVRPLARSHVALLSAAFFMVFG SEQ.ID.NO.: 47
172 GLLPVMGWNCLRDESTCSVVRPLTKNNAAILSVSFLFMFA SEQ.ID.NO.: 48
250 260 270 280
208 IMLQLYAQICRIVCRHAQQIALQRHLLPASHYVATRKGIA SEQ.ID.NO.: 46
240 IMLHLYVRICQVVWRHAHQIALQQHCLAPPHLAATRKGVG SEQ.ID.NO.: 47
212 LMLQLYIQICKIVMRHAHQIALQHHFLATSHYVTTRKGVS SEQ.ID.NO.: 48
290 300 310 320
248 TLAVVLGAFAACWLPFTVYCLLGDAHSPPLYTYLTLLPAT SEQ.ID.NO.: 46
280 TLAVVLGTFGASWLPFAIYCVVGSHEDPAVYTYATLLPAT SEQ.ID.NO.: 47
252 TLAIILGTFAACWMPFTLYSLIADYTYPSIYTYATLLPAT SEQ.ID.NO.: 48
330 340 350 360
288 YNSMINPIIYAFRNQDVQKVLWAVCCCCSSSKIPFRSRSP SEQ.ID.NO.: 46
320 YNSMINPIIYAFRNQEIQRALWLLLCGCFQSKVPFRSRSP SEQ.ID.NO.: 47
292 YNSIINPVIYAFRNQEIQKALCLICCGCIPSSLAQRARSP SEQ.ID.NO.: 48
328 SDV SEQ.ID.NO.: 46
360 SEV SEQ.ID.NO.: 47
332 SDV SEQ.ID.NO.: 48

Figure 5B


10 20 30 40
1 MNESRWTEWRILNMSSGIVNVSERHSCPLGFGHYSVVDVC SEQ.ID.NO.: 19
1 MNST-------LD-----GNQSSHPFCLLAFGY------- SEQ.ID.NO.: 15
50 60 70 80
41 IFETVVIVLLTFLII--------AGNLTVIFVFHCAPLLH SEQ.ID.NO.: 19
22 -LETVNFCLLEVLIIVFLTVLIISGNIIVIFVFHCAPLLN SEQ.ID.NO.: 15
90 100 110 120
73 HYTTSYFIQTMAYADLFVGVSCLVPTLSLLHYSTGVHESL SEQ.ID.NO.: 19
61 HHTTSYFIQTMAYADLFVGVSCVVPSLSLLHHPLPVEESL SEQ.ID.NO.: 15
130 140 150 160
113 TCQVFGYIISVLKSVSMACLACISVDRYLAITKPLSYNQL SEQ.ID.NO.: 19
101 TCQIFGFVVSVLKSVSMASLACISIDRYIAITKPLTYNTL SEQ.ID.NO.: 15
170 180 190 200
153 VTPCRLRICIILIWIYSCLIFLPSFFGWGKPGYHGDIFEW SEQ.ID.NO.: 19
141 VTPWRLRLCIFLIWLYSTLVFLPSFFHWGKPGYHGDVFQW SEQ.ID.NO.: 15
210 220 230 240
193 CATSWLTSAYFTGFIVCLLYAPAAFVVCFTYFHIFKICRQ SEQ.ID.NO.: 19
181 CAESWHTDSYFTLFIVMMLYAPAALIVCFTYFNIFRICQQ SEQ.ID.NO.: 15
250 260 270 280
233 HTKEINDRRARFPSHEVDSSRETGHSPDRRYAMVLFRITS SEQ.ID.NO.: 19
221 HTKDISERQARFSSQSGETG-EVQACPDKRYAMVLFRITS SEQ.ID.NO.: 15
290 300 310 320
273 VFYMLWLPYIIYFLLESSRVLDNPTLSFLTTWLAISNSFC SEQ.ID.NO.: 19
260 VFYILWLPYIIYFLLESSTGHSNRFASFLTTWLAISNSFC SEQ.ID.NO.: 15
330 340 350 360
313 NCVIYSLSNSVFRLGLRRLSETMCTSCMCVKDQEAQEP-- SEQ.ID.NO.: 19
300 NCVIYSLSNSVFQRGLKRLSGAMCTSC--ASQTTANDPYT SEQ.ID.NO.: 15
370
351 -KPRKRANSCSI SEQ.ID.NO.: 19
338 VRSKGPLNGCHI SEQ.ID.NO.: 15

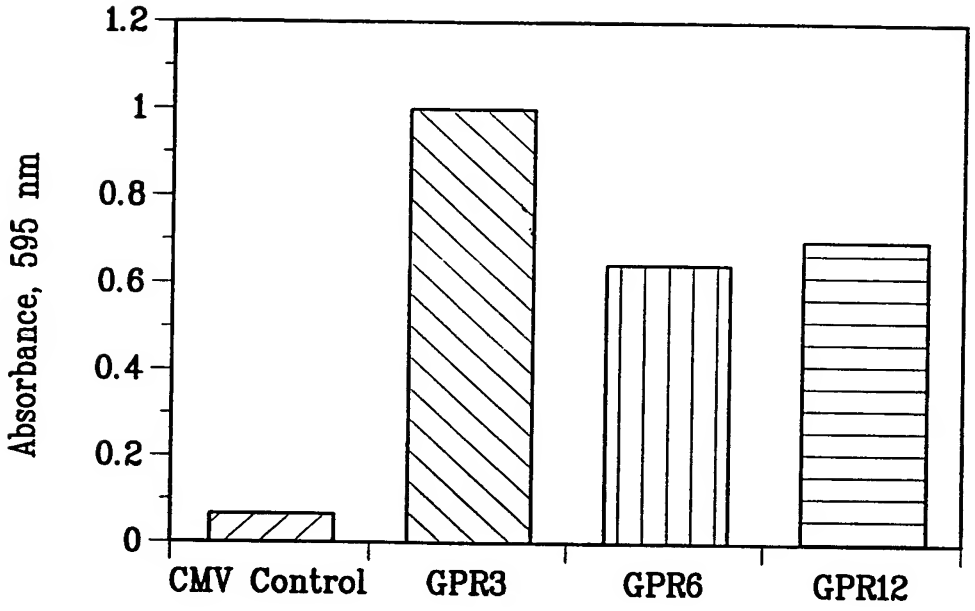

Absorbance, 595 nm
1.2
1
0.8
0.6
0.4
0.2
0
CMV Control
GPR3
GPR6
GPR12

FIG. 6A

FIG. 6B

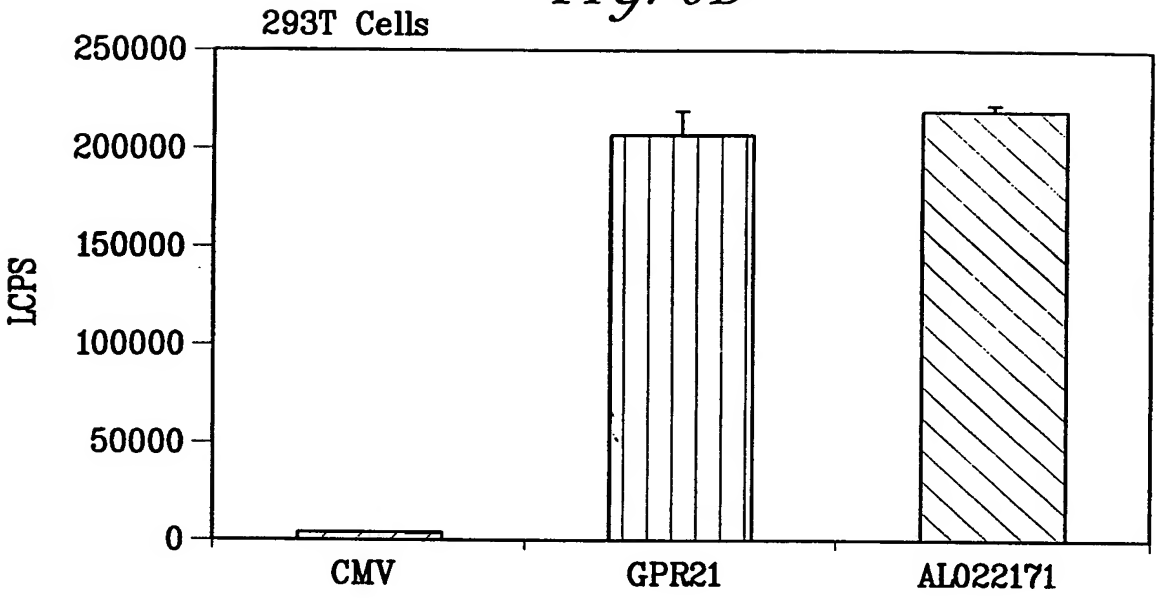

293T Cells
LCPS
250000
200000
150000
100000
50000
0
CMV
GPR21
AL022171

FIG. 6C

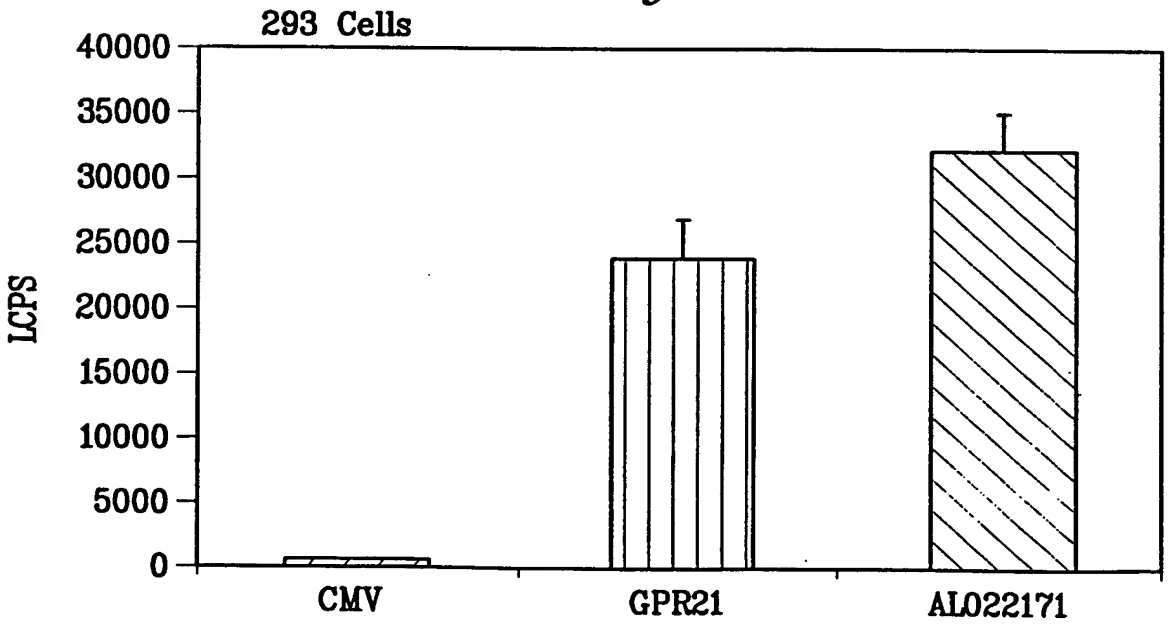
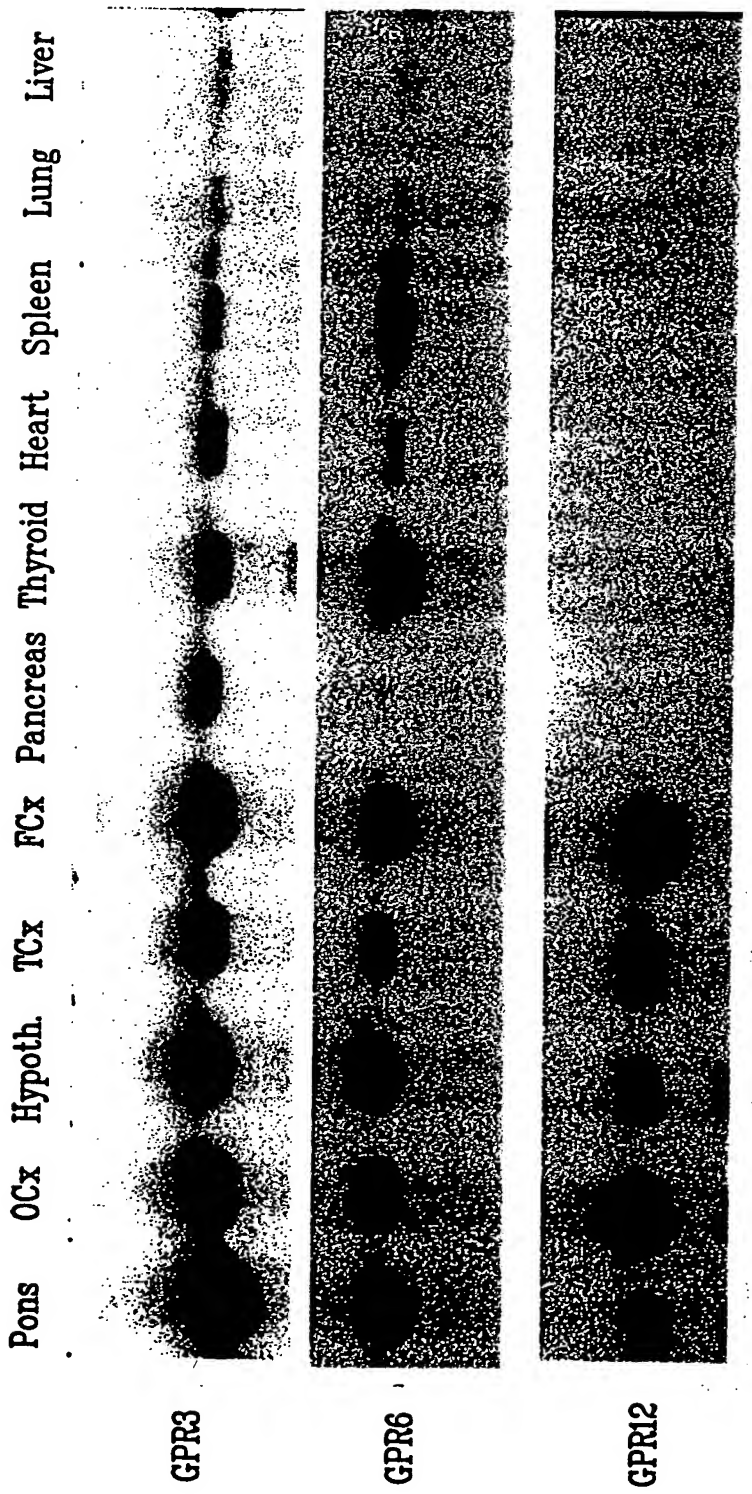

293 Cells
LCPS
40000
35000
30000
25000
20000
15000
10000
5000
0
CMV
GPR21
AL022171

FIG. 7A

FIG. 7B

FIG. 7C



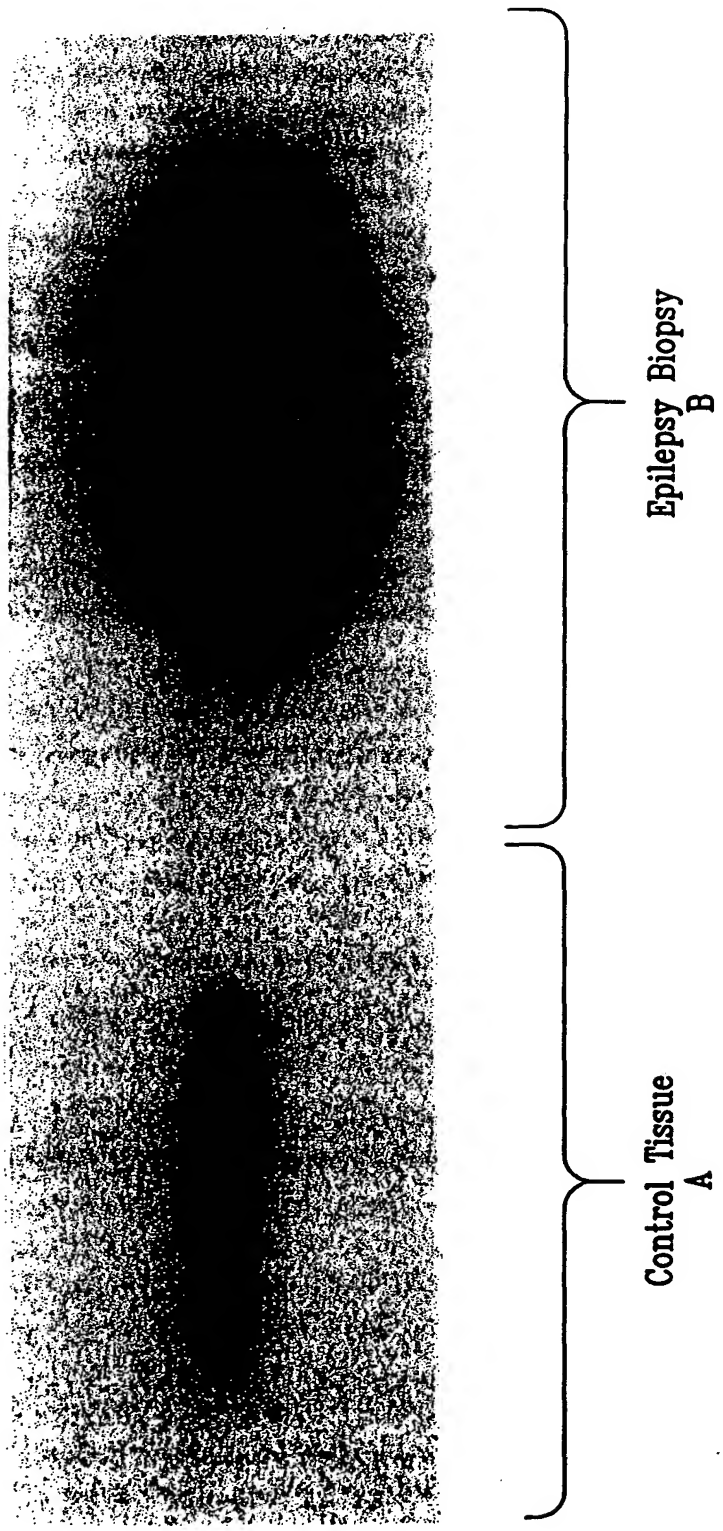


FIG. 8

FIG. 9

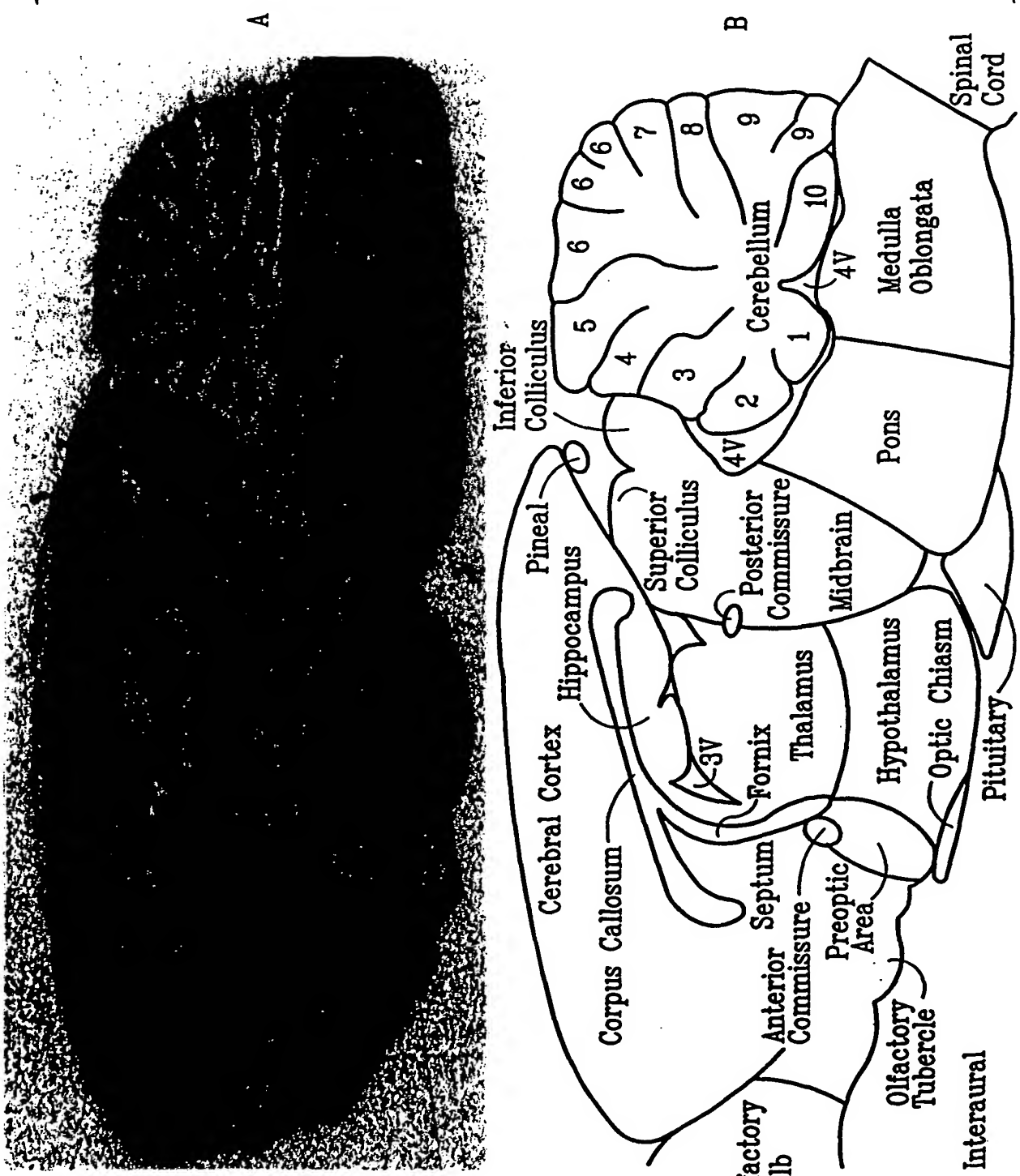

A
B
Olfactory Bulb
Anterior Commissure
Olfactory Tubercle
Corpus Callosum
Septum
Preoptic Area
Cerebral Cortex
Hippocampus
3V
Fornix
Thalamus
Hypothalamus
Optic Chiasm
Pituitary
Pineal
Superior Colliculus
Posterior Commissure
Midbrain
Inferior Colliculus
4V
Pons
Cerebellum
Medulla Oblongata
Spinal Cord
Interaural
1
2
3
4
5
6
6
6
7
8
9
9
10

FIG. 10

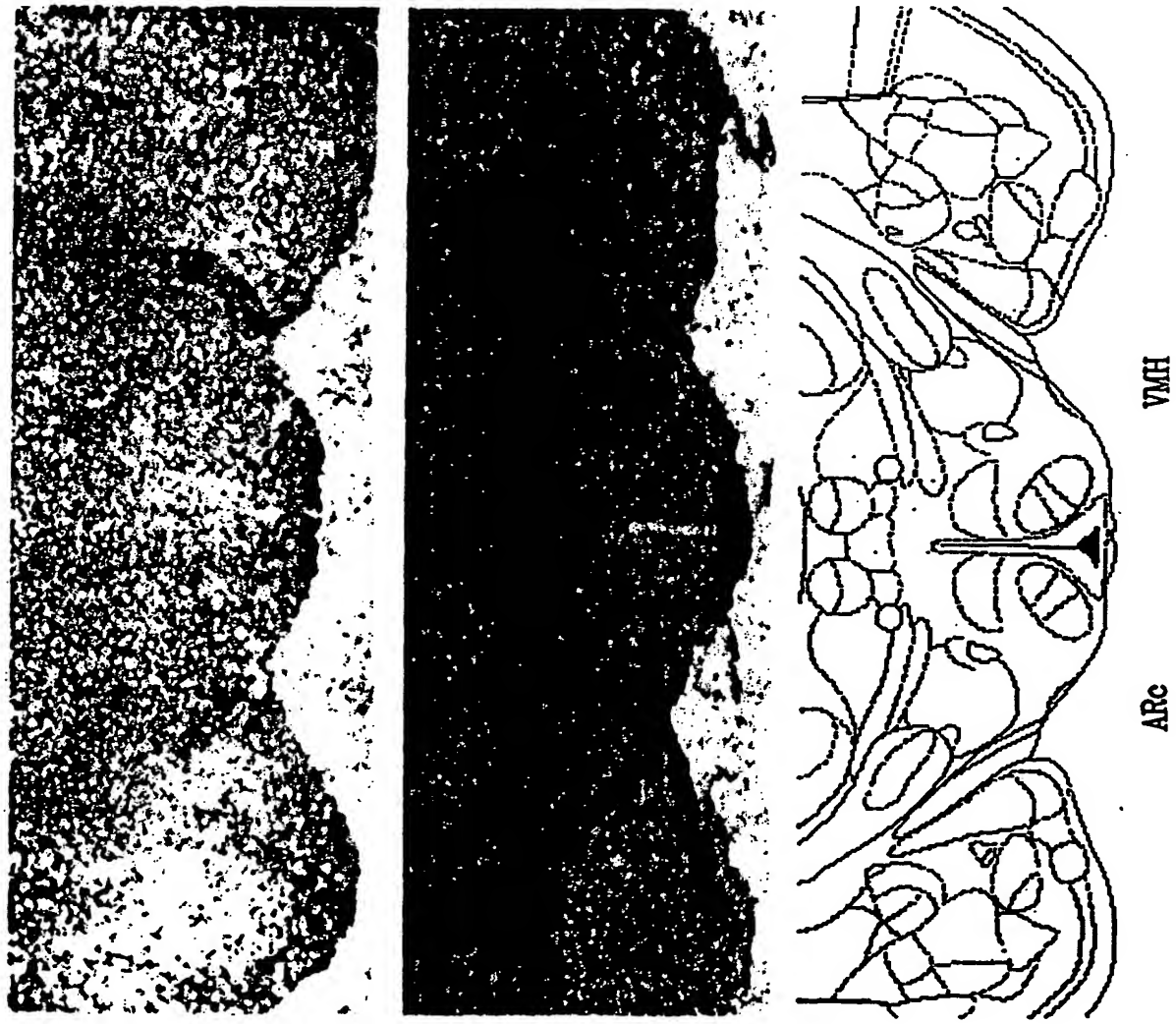


FIG. 11B

FIG. 11A

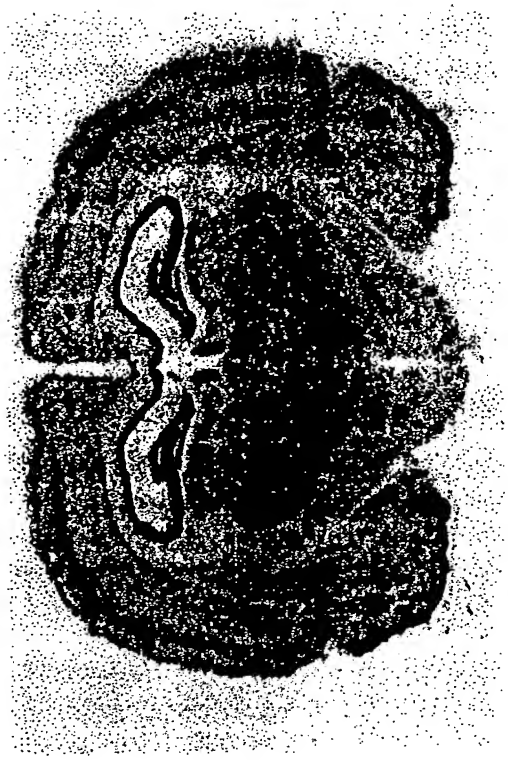


FIG. 11D

FIG. 11E

FIG. 11C

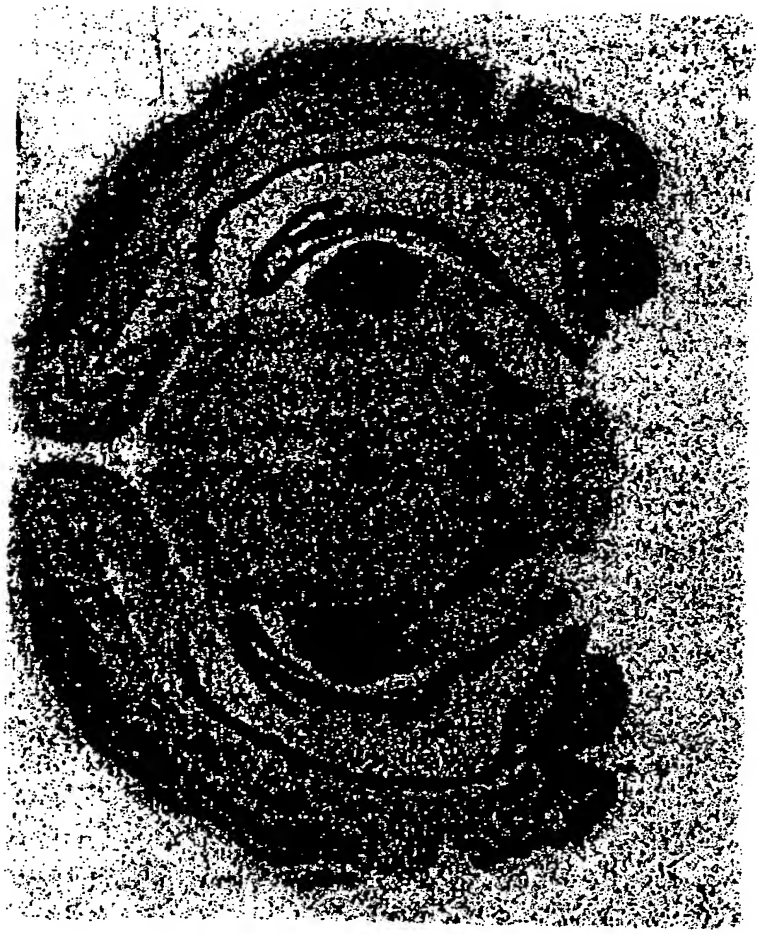


FIG. 11F

FIG. 12

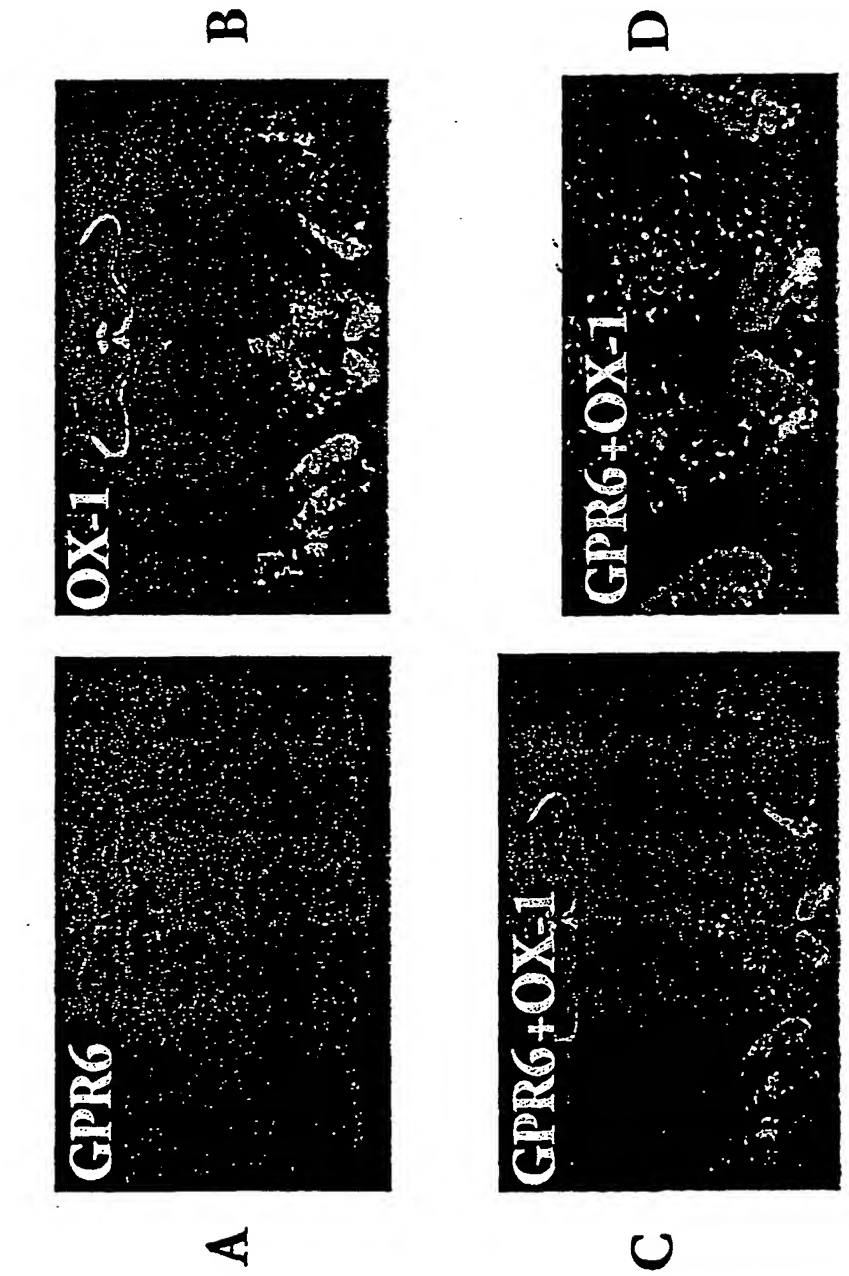
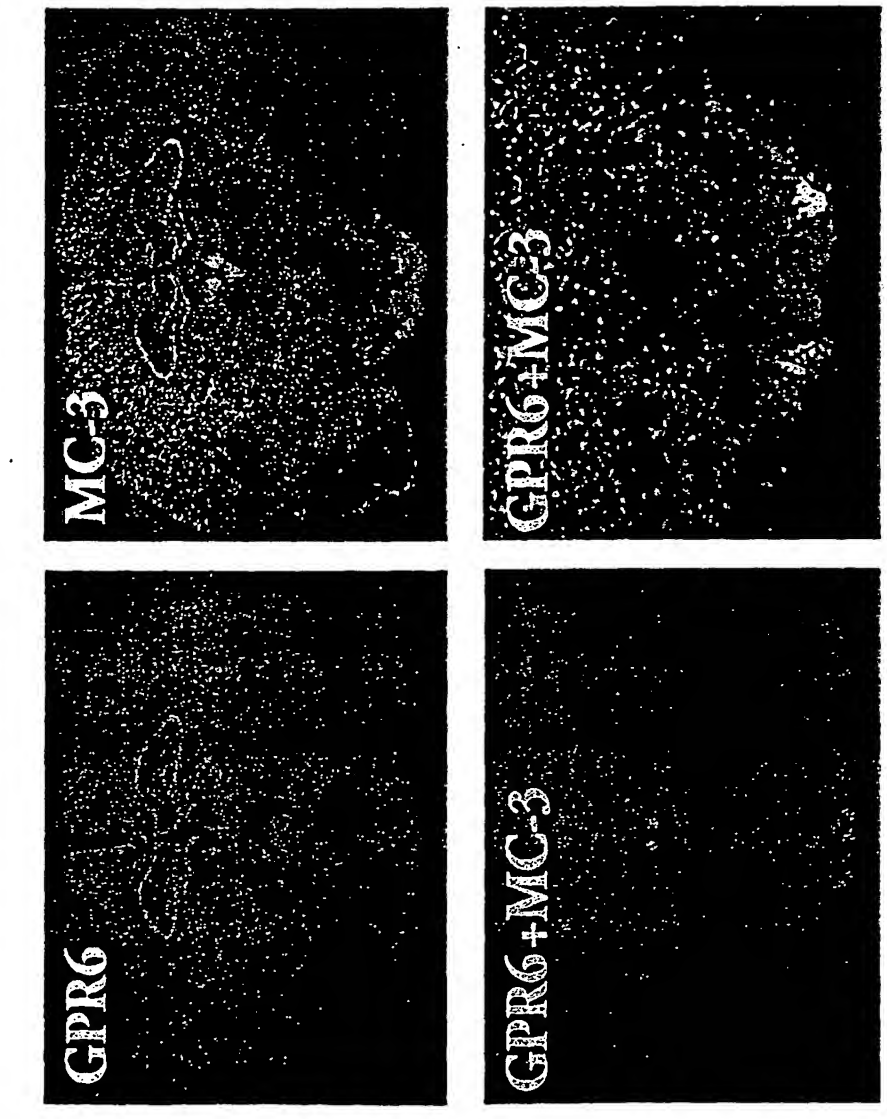


FIG. 13



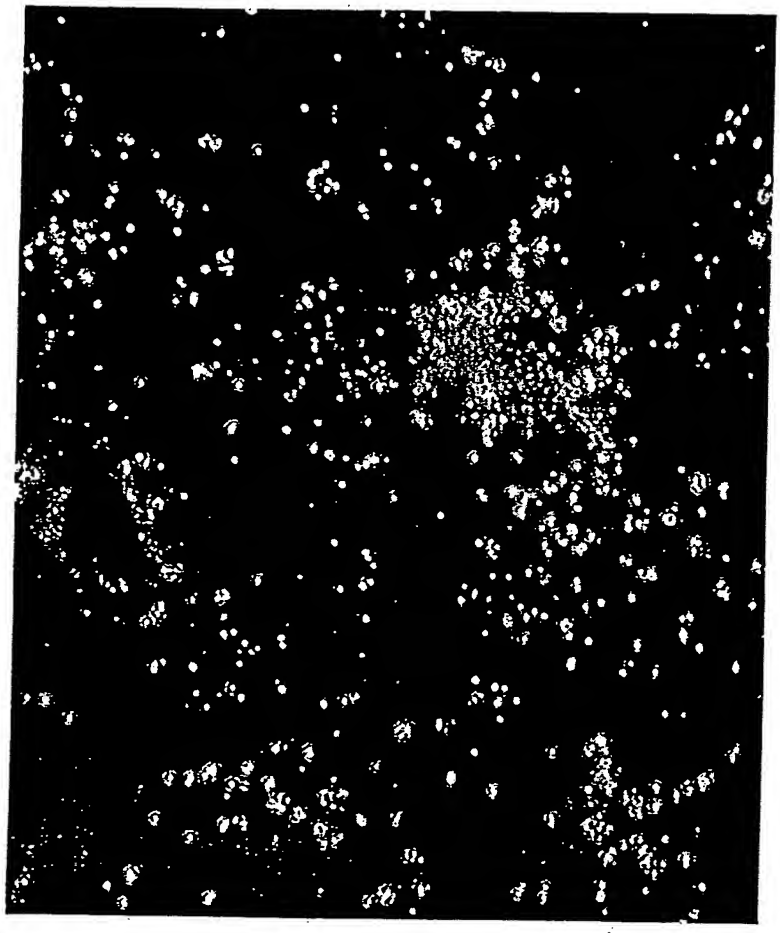


FIG. 14

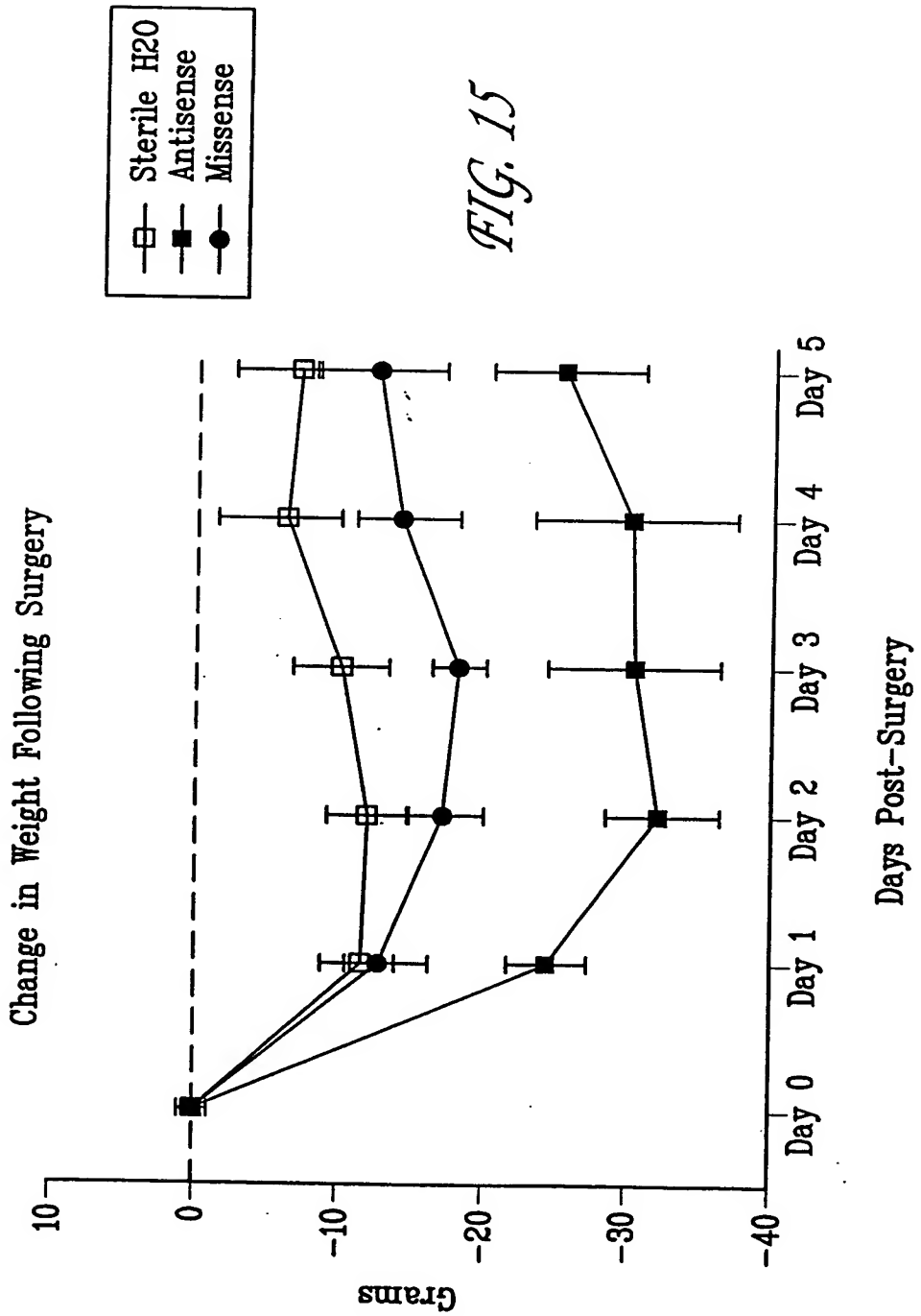

Sterile H20
Antisense
Missense
Change in Weight Following Surgery
Grams
10
0
-10
-20
-30
-40
Day 0
Day 1
Day 2
Day 3
Day 4
Day 5
Days Post-Surgery

FIG. 15

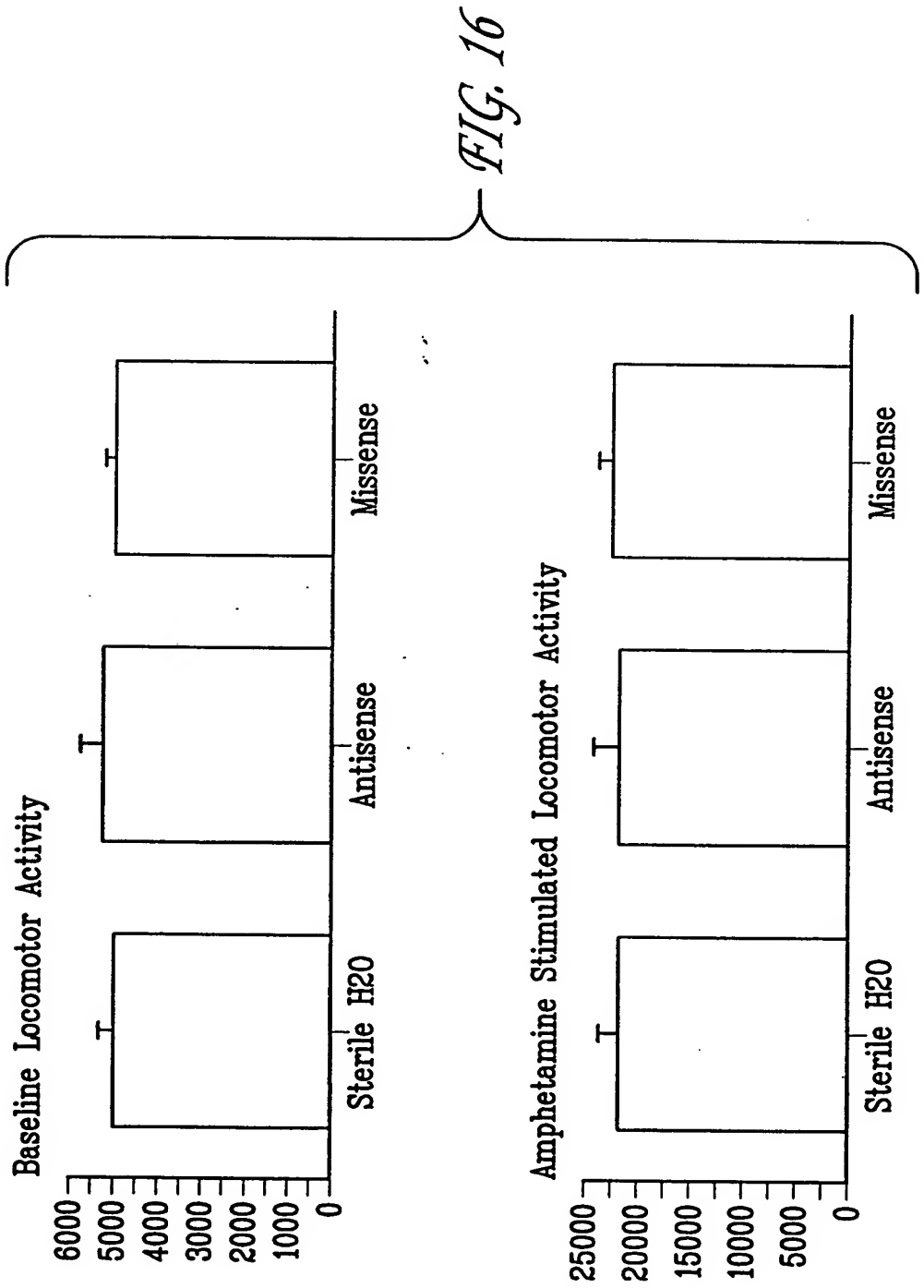

Baseline Locomotor Activity
6000
5000
4000
3000
2000
1000
0
Sterile H2O
Antisense
Missense
Amphetamine Stimulated Locomotor Activity
25000
20000
15000
10000
5000
0
Sterile H2O
Antisense
Missense

FIG. 16

FIG. 17A

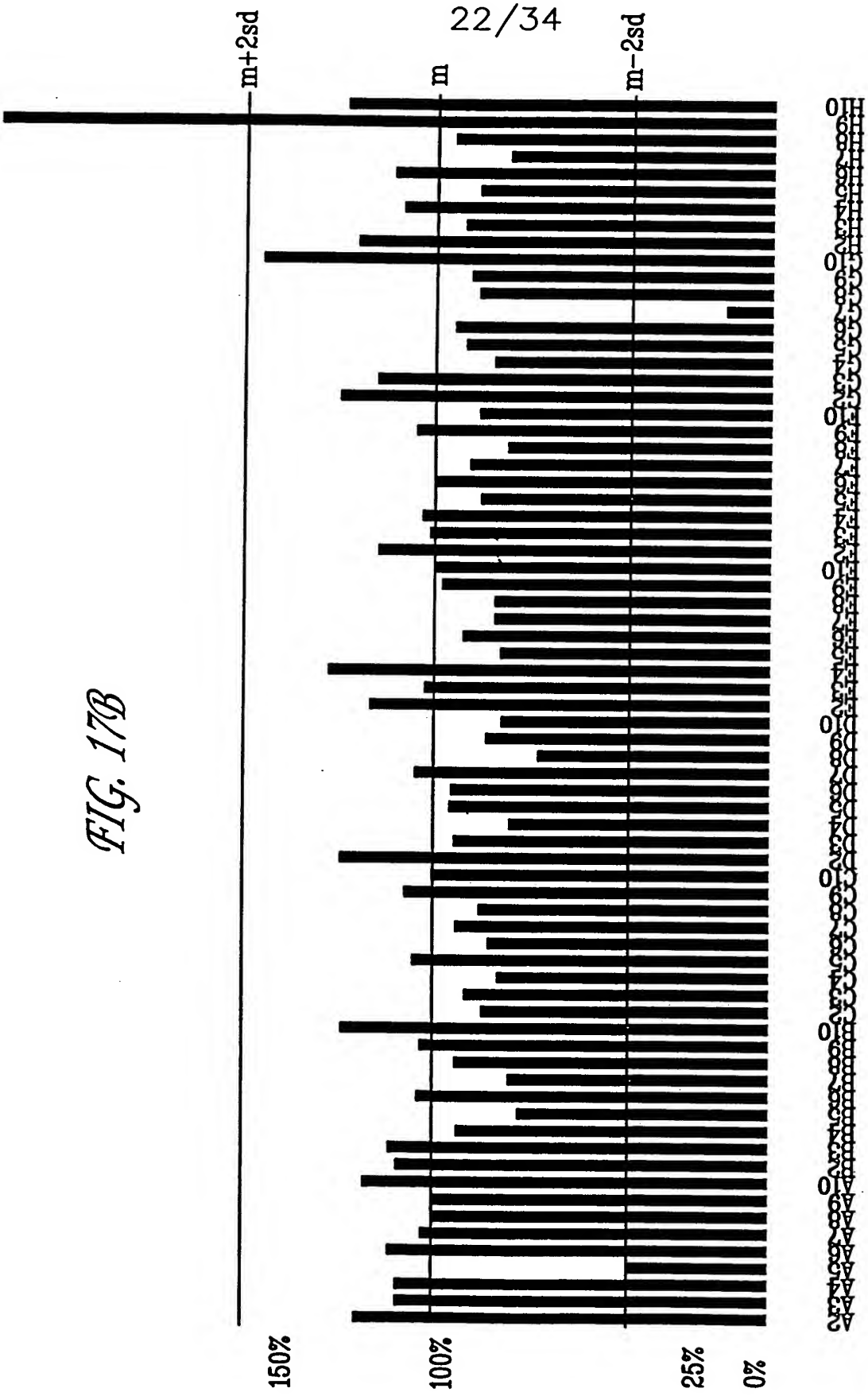


FIG. 17B

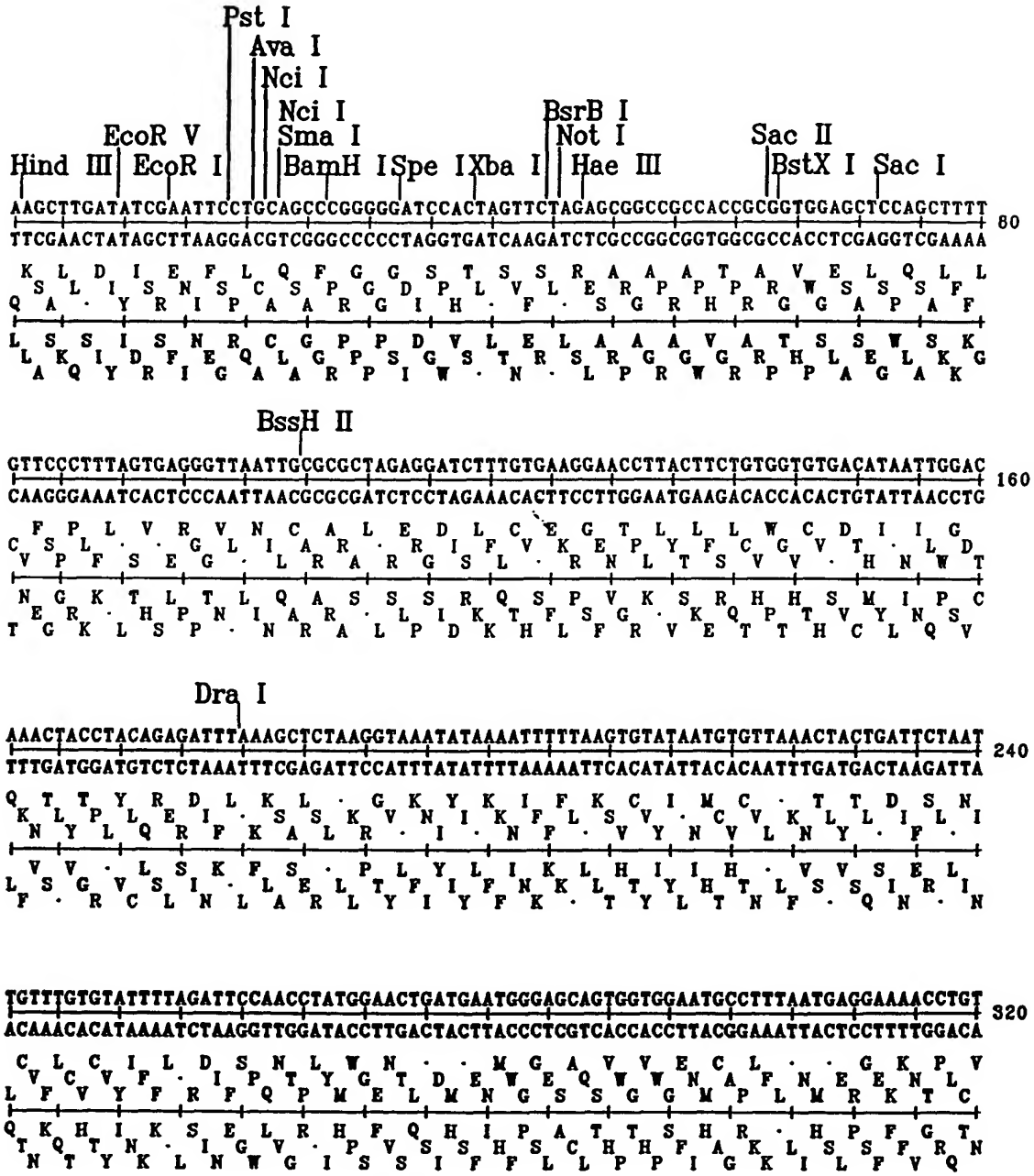

Pst I
Ava I
Nci I
Nci I
Sma I
BsrB I
Not I
EcoR V
Hind III
EcoR I
BamH I
Spe I
Xba I
Hae III
Sac II
BstX I
Sac I
BssH II
Dra I
AAGCTTGATATCGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAGCTTTT
TTCGAACTATAGCTTAAGGACGTCGGGCCCCCTAGGTGATCAAGATCTCGCCGGCGGTGGCGCCACCTCGAGGTCGAAAA
GTTCCCTTTAGTGAGGGTTAATTGCGCGCTAGAGGATCTTTGTGAAGGAACCTTACTTCTGTGGTGTGACATAATTGGAC
CAAGGGAAATCACTCCCAATTAACGCGCGATCTCCTAGAAACACTTCCTTGGAATGAAGACACCACACTGTATTAACCTG
AAACTACCTACAGAGATTTAAAGCTCTAAGGTAAATATAAAATTTTTAAGTGTATAATGTGTTAAACTACTGATTCTAAT
TTTGATGGATGTCTCTAAATTTCGAGATTCCATTTATATTTTAAAAATTCACATATTACACAATTTGATGACTAAGATTA
TGTTTGTGTATTTTAGATTCCAACCTATGGAACTGATGAATGGGAGCAGTGGTGGAATGCCTTTAATGAGGAAAACCTGT
ACAAACACATAAAATCTAAGGTTGGATACCTTGACTACTTACCCTCGTCACCACCTTACGGAAATTACTCCTTTTGGACA

FIG. 18A

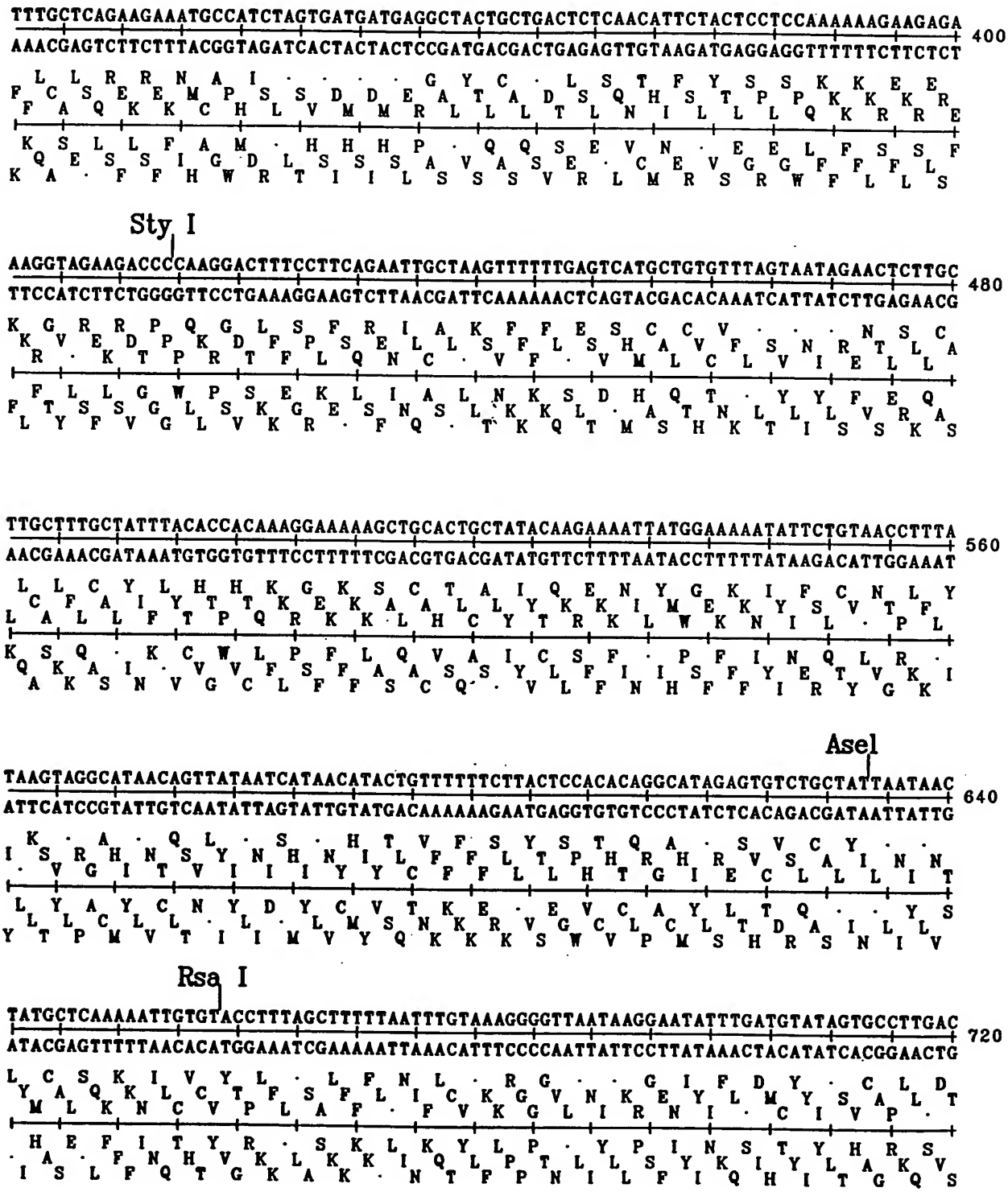


FIG. 18B

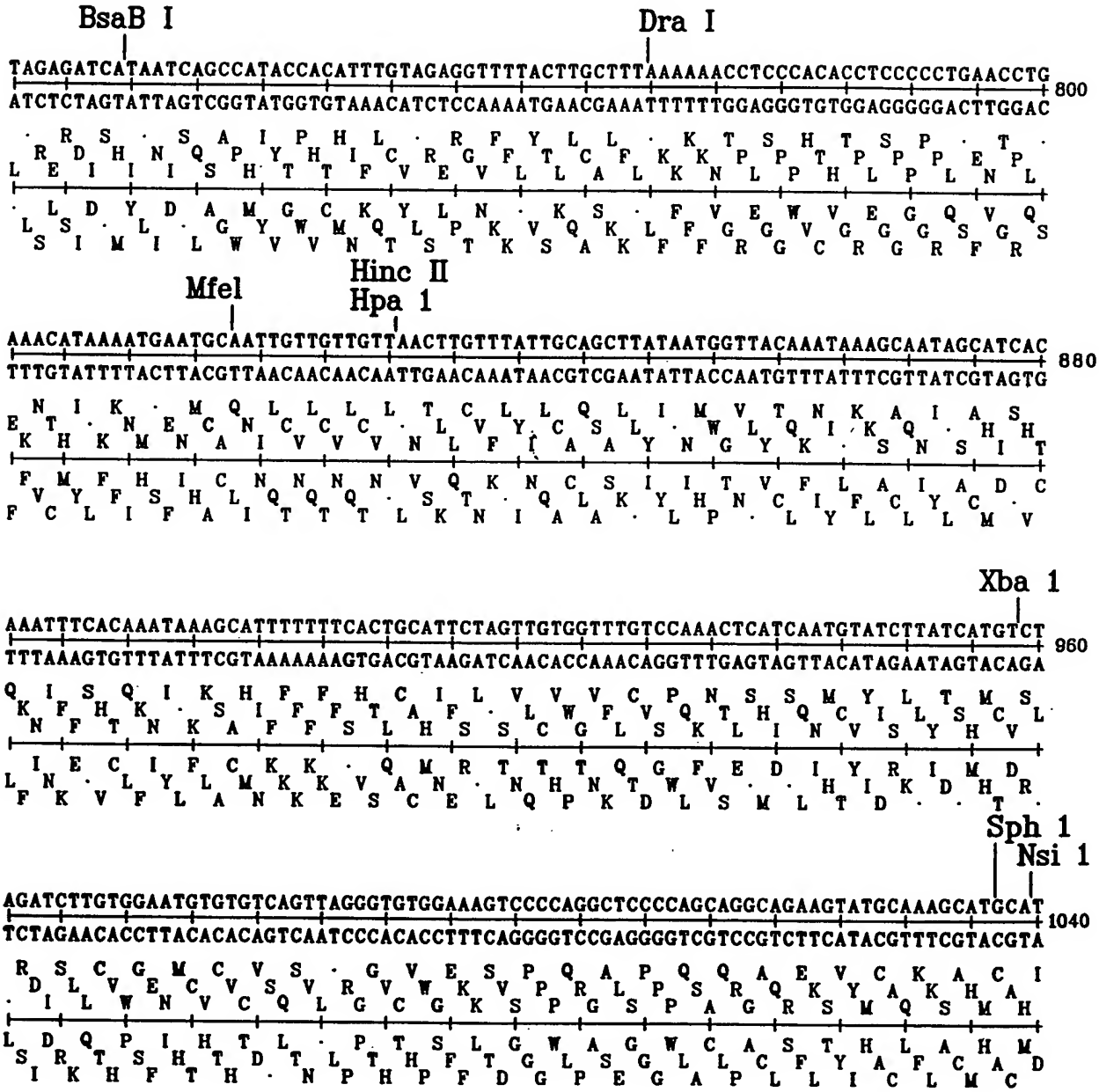


FIG. 18C

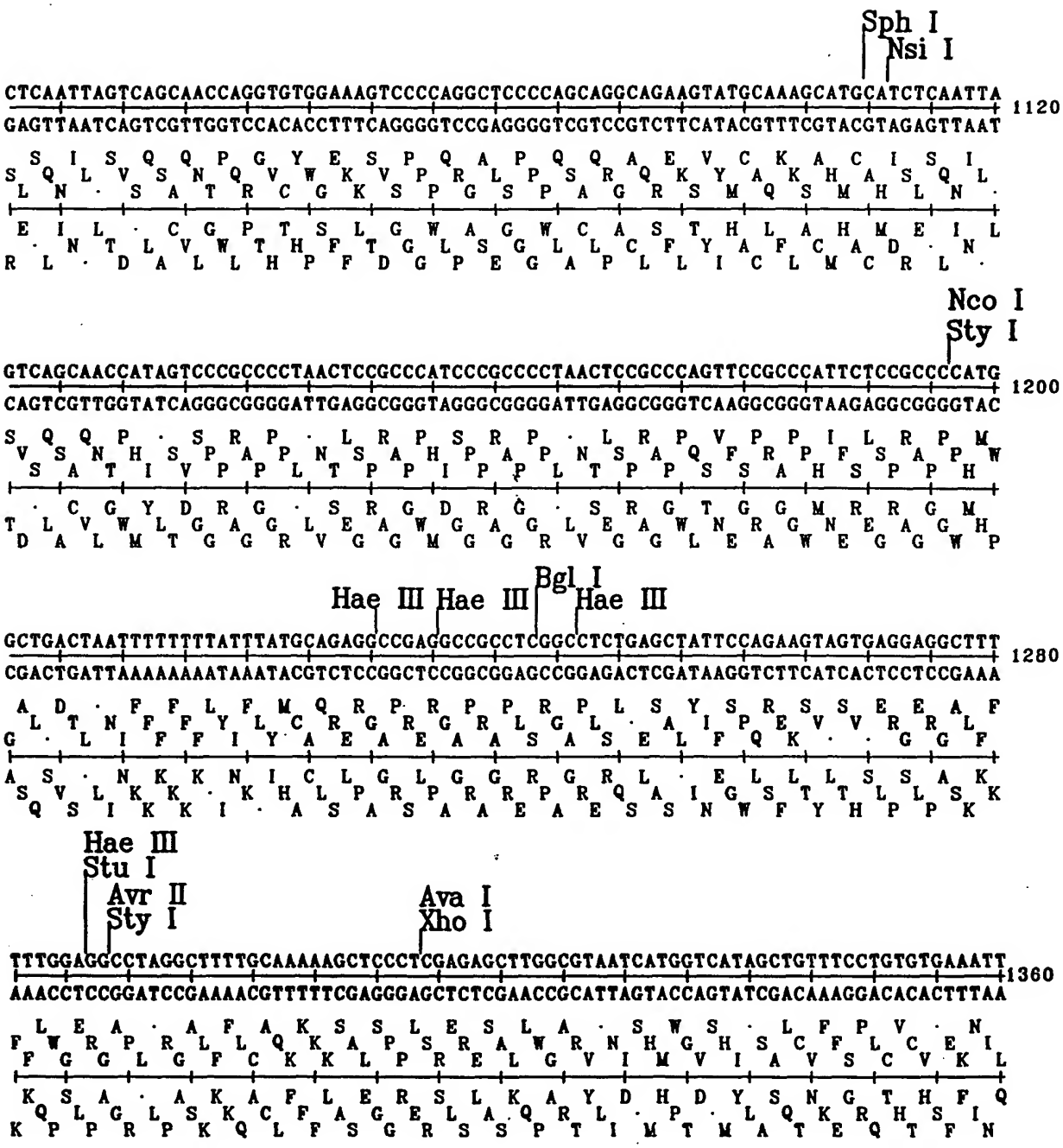

Sph I
Nsi I
CTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTA
GAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAAT
1120
Nco I
Sty I
GTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATG
CAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTAC
1200
Hae III
Hae III
Bgl I
Hae III
GCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTT
CGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAA
1280
Hae III
Stu I
Avr II
Sty I
Ava I
Xho I
TTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATT
AAACCTCCGGATCCGAAAACGTTTTTCGAGGGAGCTCTCGAACCGCATTAGTACCAGTATCGACAAAGGACACACTTTAA
1360

FIG. 18D

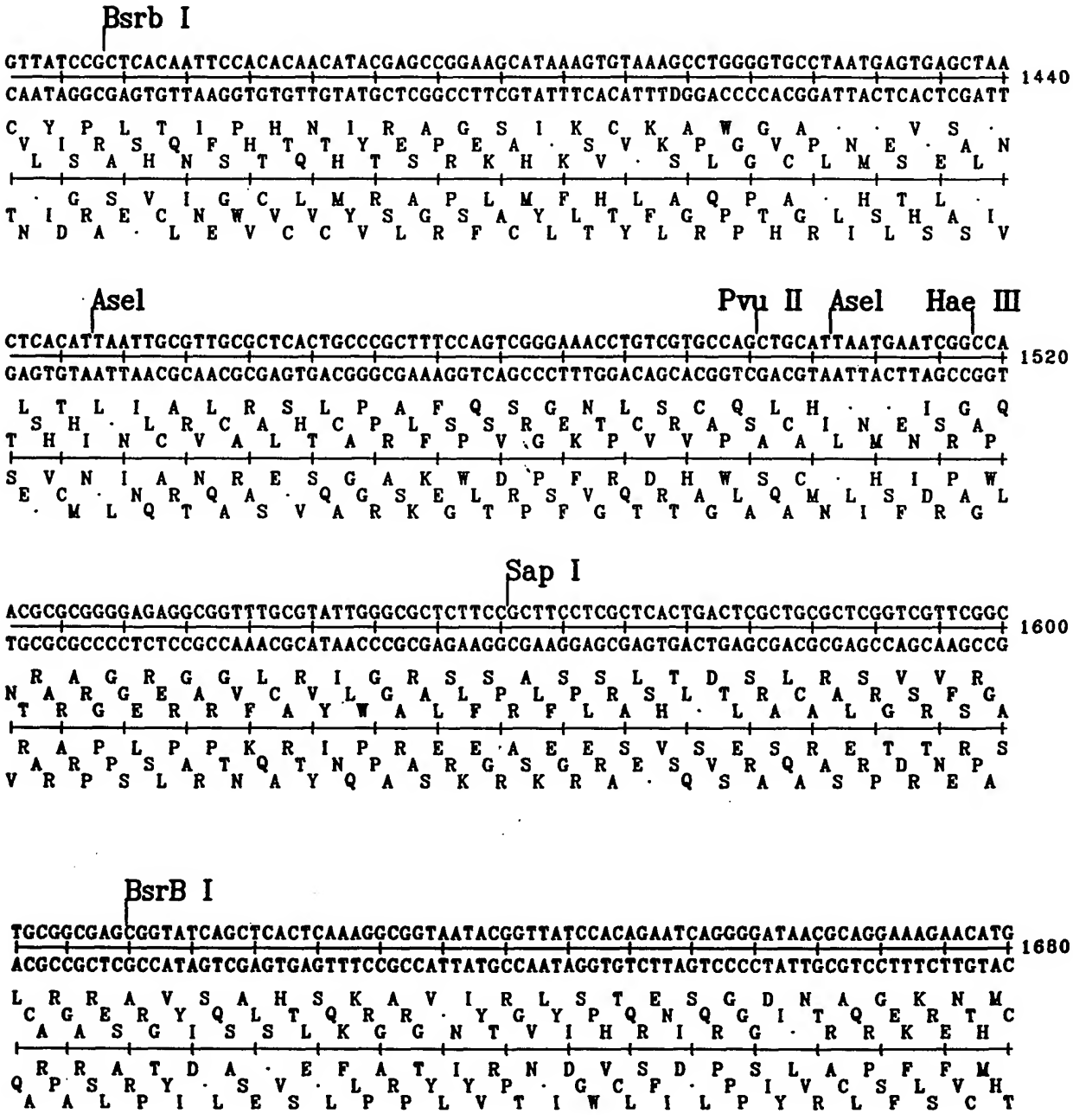

Bsrb I
GTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAA
CAATAGGCGAGTGTTAAGGTGTGTTGTATGCTCGGCCTTCGTATTTCACATTTDGGACCCCACGGATTACTCACTCGATT
1440
AseI
Pvu II
AseI
Hae III
CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA
GAGTGTAATTAACGCAACGCGAGTGACGGGCGAAAGGTCAGCCCTTTGGACAGCACGGTCGACGTAATTACTTAGCCGGT
1520
Sap I
ACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGC
TGCGCGCCCCTCTCCGCCAAACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCG
1600
BsrB I
TGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATG
ACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGTAC
1680

FIG. 18E

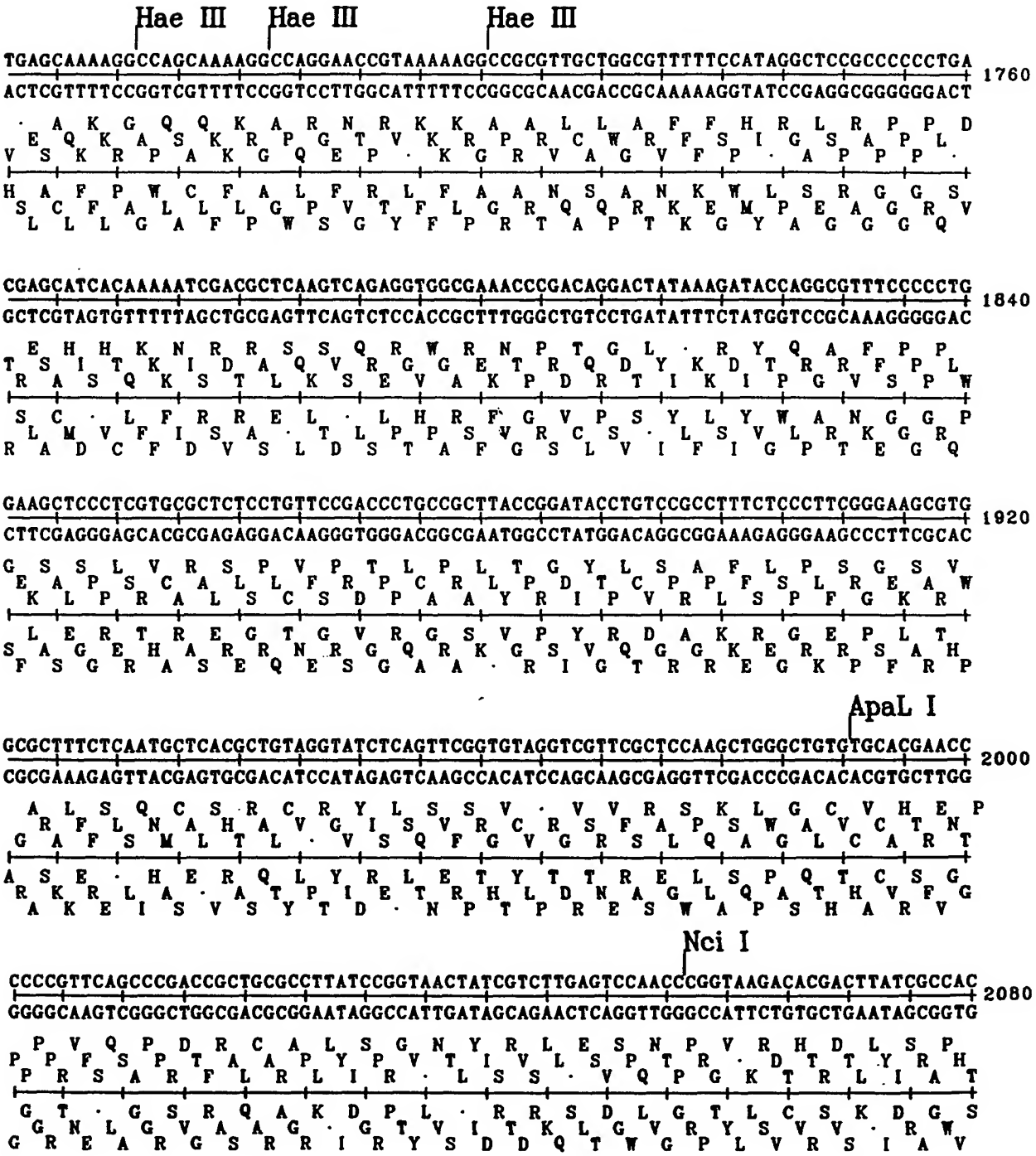


FIG. 18F

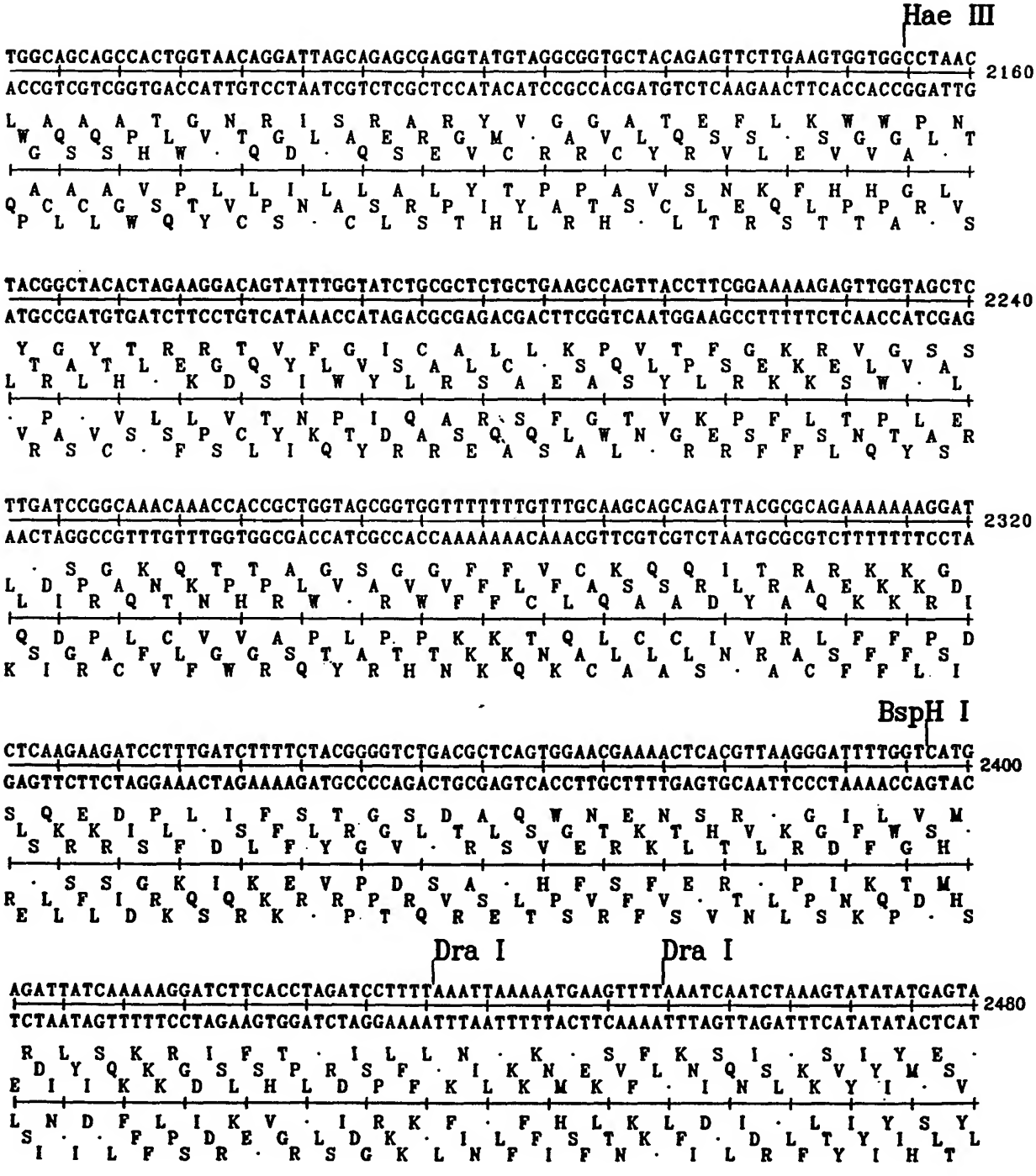


FIG. 18G

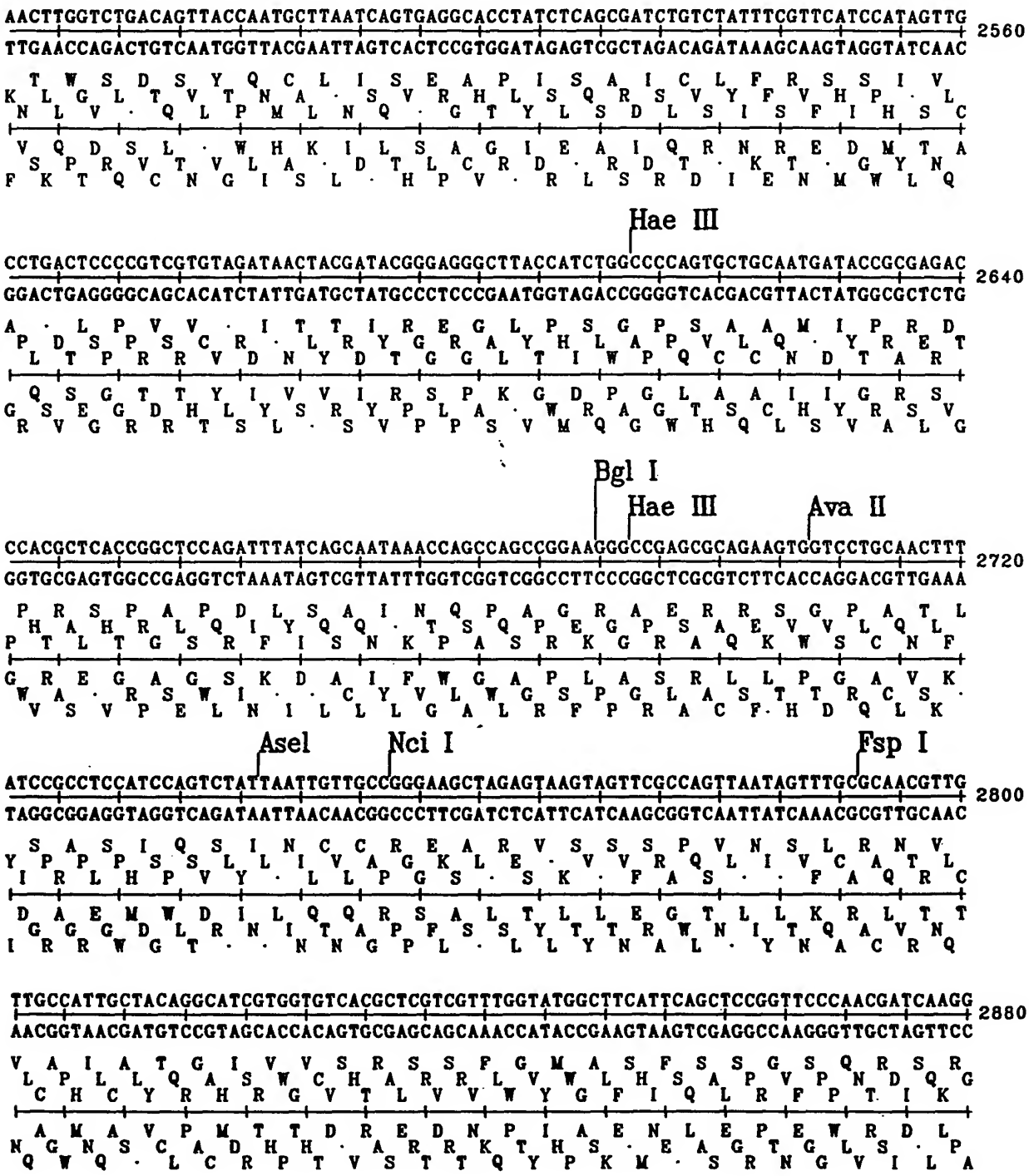

Hae III
Bgl I
Hae III
Ava II
AseI
Nci I
Fsp I
2560
2640
2720
2800
2880

FIG. 18H

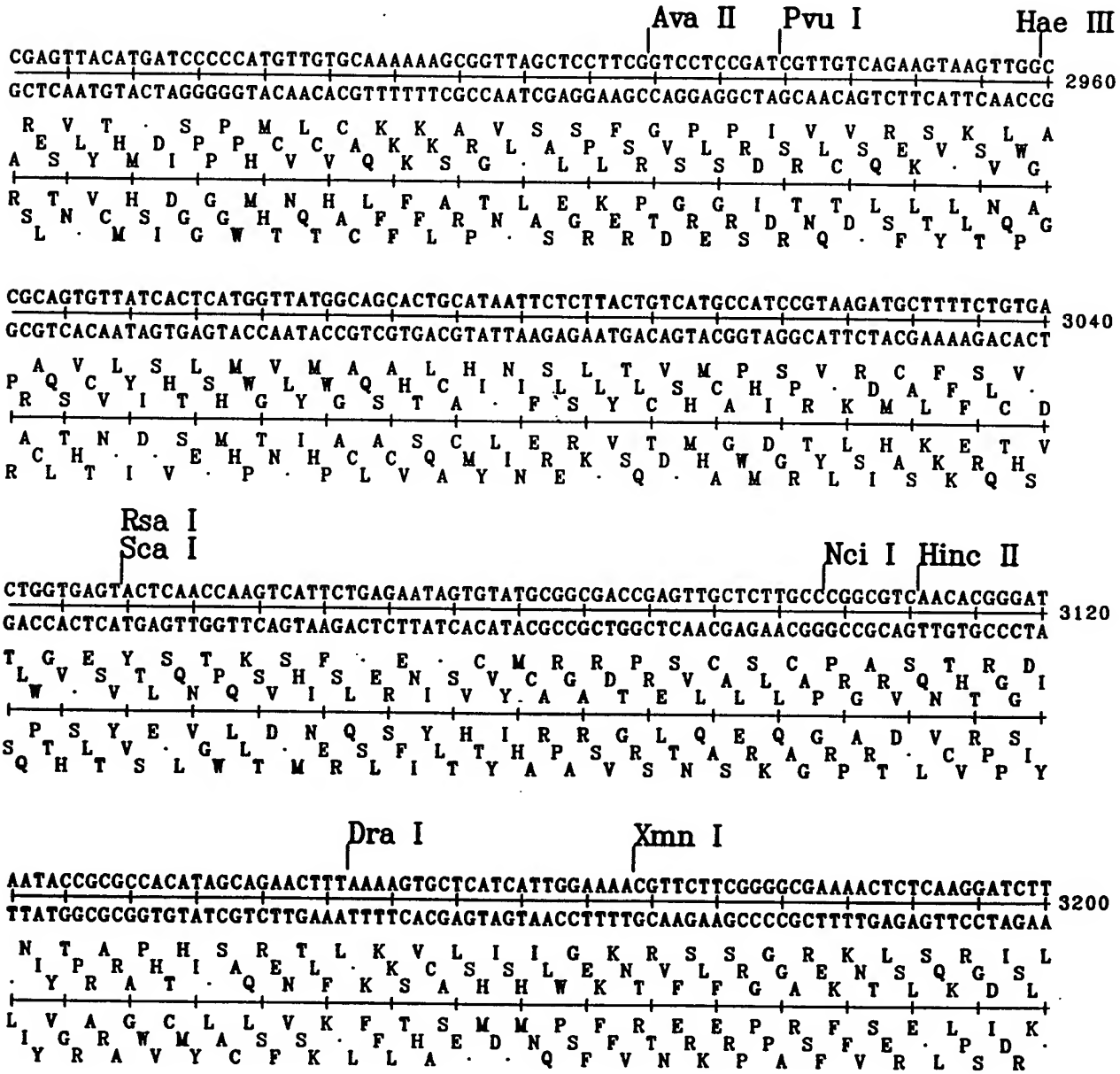

Ava II
Pvu I
Hae III
Rsa I
Sca I
Nci I
Hinc II
Dra I
Xmn I
2960
3040
3120
3200

FIG. 18I

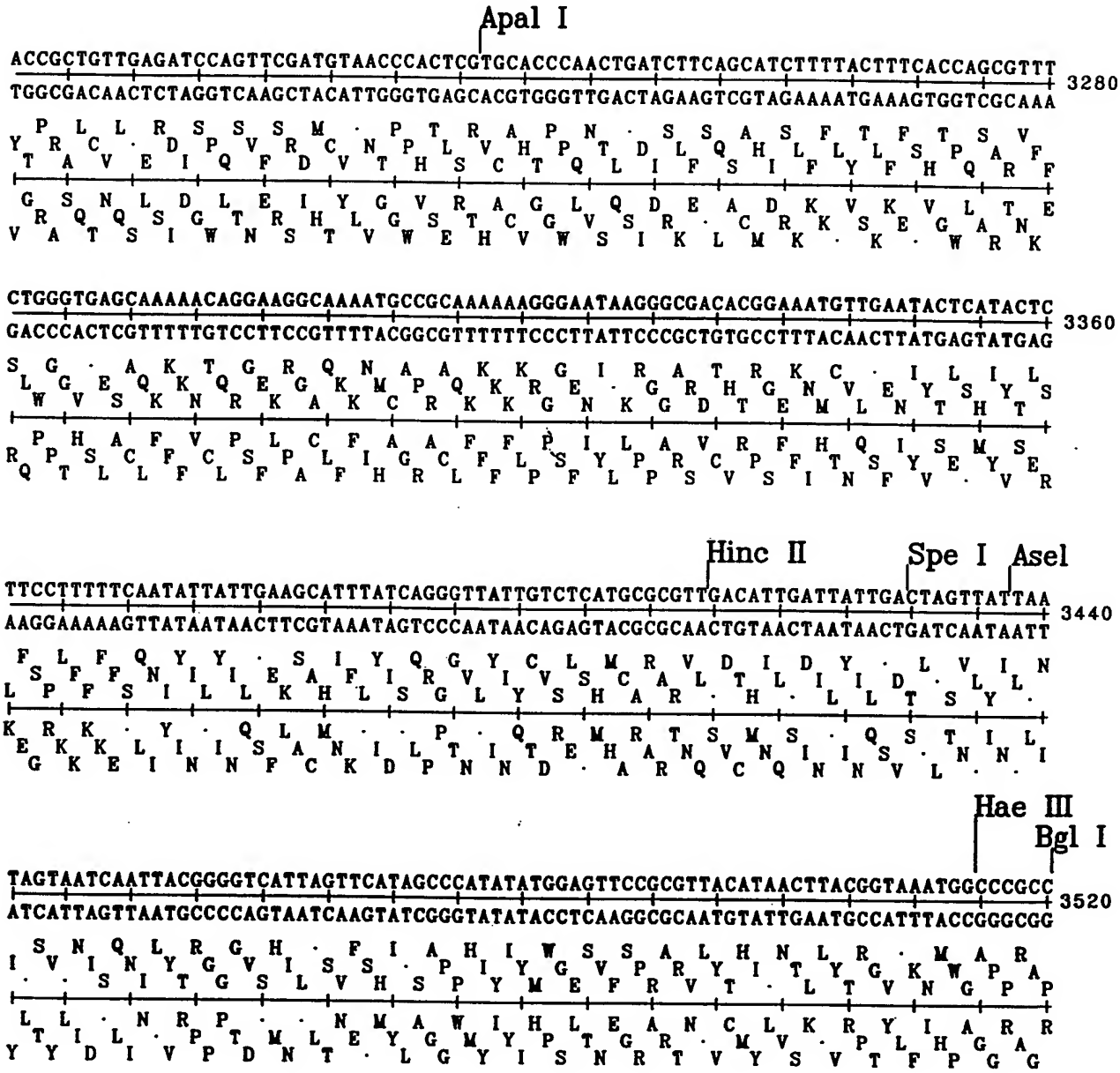


FIG. 18J

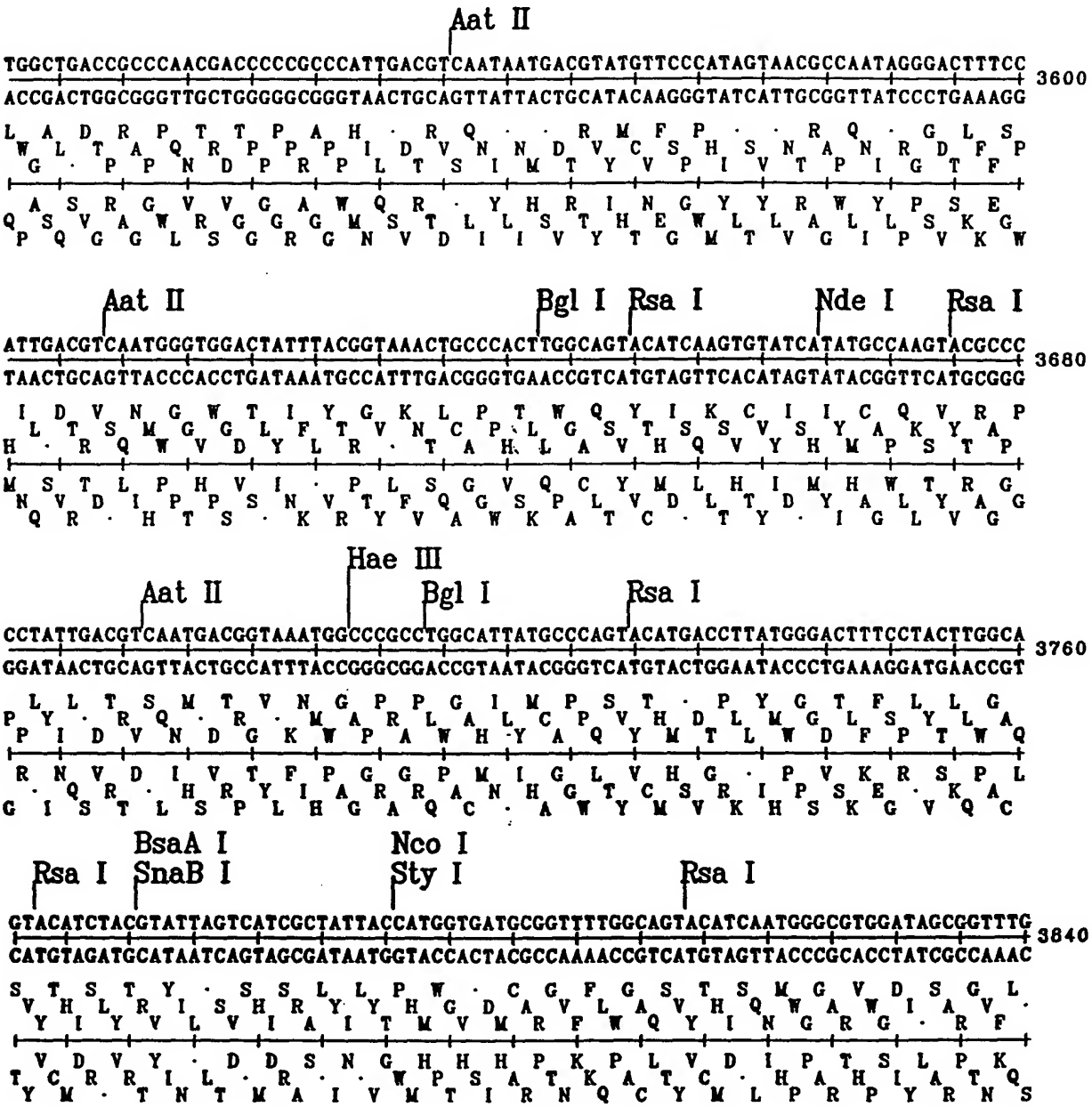

Aat II
TGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC 3600
ACCGACTGGCGGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGG
Aat II
Bgl I
Rsa I
Nde I
Rsa I
ATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCC 3680
TAACTGCAGTTACCCACCTGATAAATGCCATTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGG
Hae III
Aat II
Bgl I
Rsa I
CCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCA 3760
GGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCATGTACTGGAATACCCTGAAAGGATGAACCGT
BsaA I
SnaB I
Nco I
Sty I
Rsa I
Rsa I
GTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTG 3840
CATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCTATCGCCAAAC

FIG. 18K

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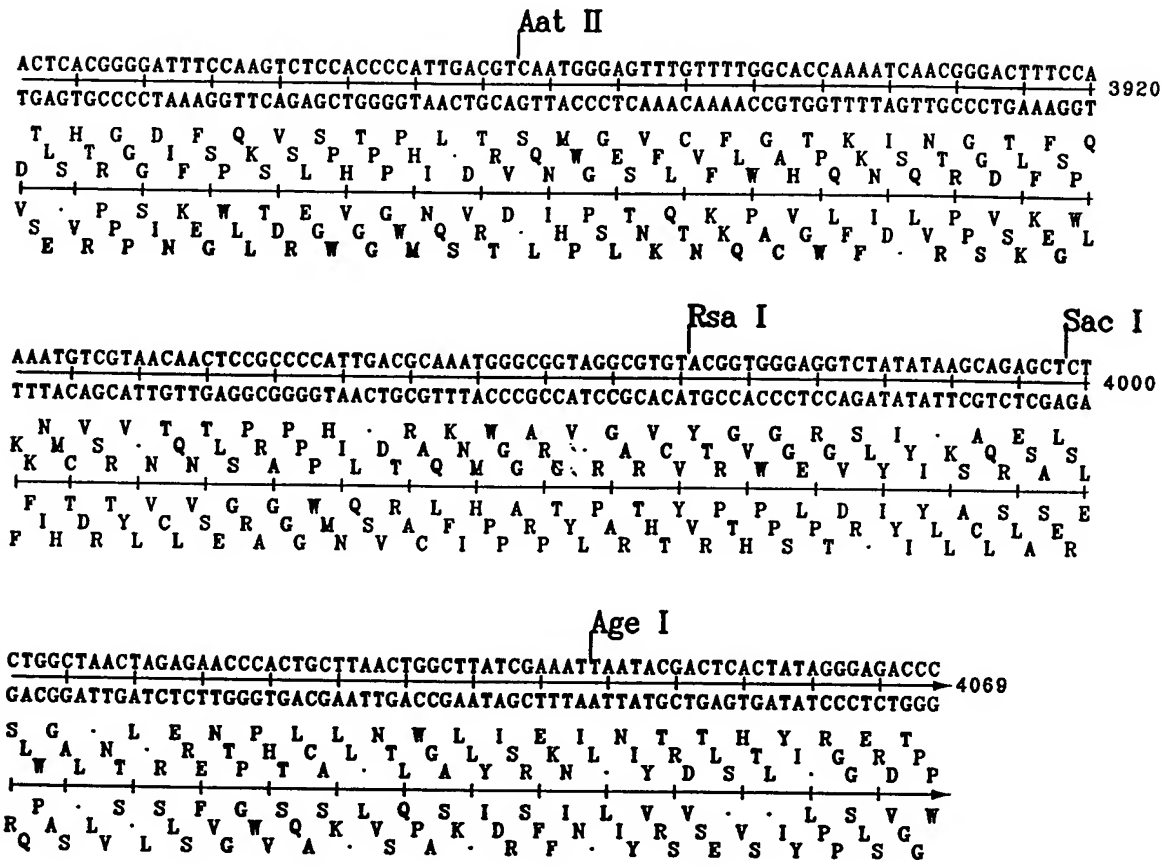

FIG. 18L